133, App 132, App 1, Appli

Sequence Sequence Sequence Sequence Sequence Sequence

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Title: Perfect score: Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Database

Result

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APPLICANT: RAFF, Mitchell E.
APPLICANT: KLOSTZER, William S.
APPLICANT: MICHARDAN, TARCHIKO, TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3; Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ANILOLAGE AND NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: P.O. Box 1404
CITY: Alexandria
STREET: P.O. Box 1404
COUNTRY: United States
ZIS: ALEADALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/803,085
FILING DATE: 20 FPEB-1997
CLASSIFICATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELECOMMUNICATION POR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
L'ENGTH: 390 base pairs
                                                                                                            US-08-652-816A-27
US-08-665-202-4
US-09-315-574-4
US-09-240-274-133
                                                             US-09-526-098-9
US-09-049-672A-25
US-09-079-029-8
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US-08-199-911-1
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US-08-264-093-5
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                                                                                                                                                                                                                                     JS-10-039-785-62
                              -08-345-321-3
-08-487-550-9
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                              ; Sequence 1, Applical
; Patent No. 6011138
; GENERAL INFORMATION
; APPLICANT: REFF
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; LOCATION:
US-08-803-085-1
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December 29, 2003, 16:08:50 ; Search time 42.9294 Seconds (without alignments) 4009.823 Million cell updates/sec
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
              GenCore version 5.1..6
(c) 1993 - 2003 Compugen Ltd.
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US-09-338-933-267
US-10-09-215-68-59
US-10-039-785-64
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US-08-958-201-13
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US-10-039-785-61
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                                                                                                                                                                                                                                                                                                             569978 seqs, 220691566 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                   nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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                                Copyright
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2295.2 2295.2 2285.4 2285.4 2285.4 2275.8 2275.8 2275.8 2275.2 2225.2 2252.2 2339.6 2334.6

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; LIBRARY: THYRNOT10
; CLONE: 2872705
US-09-049-672A-23
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APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                  o;
                                  0; Indels
                 Pred. No. 4.3e-106; 
; Mismatches 0;
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SOFTWARE: FREISEGO FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 GGAAGAGGACCCGGTTGACCGTCCTAGGT 390
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100.08;
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REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-O
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           incyte Pharmace.
incyte Pharmace.
CITY: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                 Best Local Similarity 100.
Matches 390; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 321.2; DB 3;
Pred. No. 1.2e-85;
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Patent No. 5976961
GENERAL INFORMATION:
APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
ITILE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              394 GGCGGAGGACCAAGCTGACCGTCCTAGGT 423
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.4%;
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 891 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 89.0
Matches 347; Conservative
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FastSEQ for Windows Version 3.0
                                                              TYPE: DNA
CRGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LCCATION: (1)...(548)
CTHER INFORMATION: n = A,T,C or G
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US-09-938-938-267
                                                                                                                                                                                                        Query Match 75.7%;
Best Local Similarity 87.7%;
Matches 343; Conservative
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Best Local Similarity 87.7
Matches 343; Conservative
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LOCATION: (1)...(548)
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ORGANISM: Homo sapien
 NUMBER OF SEQ I
SOFTWARE: Fast
SEQ ID NO 267
LENGTH: 548
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LENGTH: 548
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APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
CURRENT APPLICATION WHORER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
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Pred. No. 3.5e-85;
0; Mismatches 44
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ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTATION NUMBER: 30,37
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-640
TELEPHONE: (202) 783-6031
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 902 base pairs
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Patent No. 6468546
GENERAL INFORMATION:
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88.7%;
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Matches 346; Conservative
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89..739
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LOCATION:
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FEATURE:
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LOCATION:
US-08-378-939-11
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                                                       Gaps
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  Length 548;
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Sequence 267, Application US/09338933

Batent No. 6488931

GENERAL INFORMATION:
APPLICANT: Mitcham Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
TITLE OF INVENTION: OVARIAN CANCER;
FILE REFERENCE: 210121.462C1

CURRENT APPLICATION NUMBER: US/09/338, 933

CURRENT FILING DATE: 1999-06-23

NUMBER OF SEQ ID NOS: 312

SOFTWARE: FastSEQ for Mindows Version 3.0
                                                       Indels
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87.7%; Pred. No. 4.9e-78;
live 0; Mismatches 46;
     DB 4;
Score 295.2; DB 4;
Pred. No. 4.9e-78;
0; Mismatches 46;
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AAGCGGGCCTCAGGGGTCTCTGATCGCTTCTGGCTCCAAGTCTGGCAACACGGCCTCC 279
                                         GATCGCTTCTCTGGCTCCCAAGTCTGGCAACACGCCTCCCTGACCATCTCTGGGCTCCAG 300
                                                                                                 287 GATCGCTTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGGCTCCAA 346
                                                                                                                                                                                                                                                                                      GGACAGTCGGTCACCATCTCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTAT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-019-718-795 - Sequence 59, Application US/10039785 | Sequence 59, Application US/10039785 | Parent No. 6538938 | GENERAL INFORMATION: Antibodies that Immunospecifically Bind to TRAIL ITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL ITLE OF INVENTION: Receptors | FILE REFERENCE: PF550 | CURRENT APPLICATION NUMBER: US/10/039,785 | CURRENT FILING DATE: 2002-04-05 | PRIOR PAPLICATION NUMBER: 60/341,237 | PRIOR APPLICATION NUMBER: 60/341,237 | PRIOR APPLICATION NUMBER: 60/311,044 | PRIOR APPLICATION NUMBER: 60/31,044 | PRIOR PILING DATE: 2001-11-14 | PRIOR PILING DATE: 2001-11-09 | PRIOR PILING DATE: 2001-10-09 | PRIOR PELING DATE: 2001-10-09 | PRIOR PELING DATE: 2001-09-21 | PRIOR PELING DATE: 2001-09-21 | PRIOR PILING DATE: 2001-09-21 | PRIOR PILING DATE: 2001-09-21 | PRIOR PILING DATE: 2001-09-22 | PRIOR PILING DATE: 2001-09-20 | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                           360 CGGAAG-AGGGACCCGGTTGACCGTCCTAGG 389
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US-10-039-785-59
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Best Local Similarity
Matches 310; Conservat
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: Frudakis, Tony N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS;
TITLE OF INVENTION: OF OVARIAN CANCER;
FILE REFERENCE: 210121-1463
CURRENT APPLICATION NUMBER: US/09/215,681A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 267
LENGTH: 548
1 ATGGCCTGGACTCTGCTCCTCGTCACCTCTCAGGGCACAGGATCC
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tive 0; Mismatches 46
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Patent No. 6528253
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US-09-215-681-267
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88.3%; Pred. No. 4.2e-75;
iive 0; Mismatches 41
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US-10-039-785-64
                                                                                                                                                                                                US-10-039-785-64; Sequence 64, Application US/10039785; Patent No. 6538938; GENERAL INFORMATION:
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Matches 310; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGCCTCCAAGTCTGGCAACACGGCCTCC 624
               CTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACA 339
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                                                                                  625 crgaccarcregegerecagecreaceaceaegecrearrarracrecaecreararaca 684
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US-10-039-785-63
Sequence 63, Application US/10039785
Patent No. 6538938
GENERAL INFORMATION:
APPLICANT: Salcede a. 1.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PFSSO
CURRENT FILING DATE: 2002-04-05
FRIOR PRIOR PELICATION NUMBER: 60/349,860
PRIOR FILING DATE: 2002-04-05
PRIOR PELING DATE: 2001-12-20
PRIOR PELING DATE: 2001-11-14
PRIOR PELING DATE: 2001-11-14
PRIOR PELING DATE: 2001-11-09
PRIOR PELING DATE: 2001-11-09
PRIOR PELING DATE: 2001-10-09-21
PRIOR PELING DATE: 2001-10-09-21
PRIOR PELING DATE: 2001-09-21
PRIOR PELING DATE: 2001-09-22
PRIOR PELING DATE: 2001-09-22
PRIOR PELING DATE: 2001-06-04
PRIOR PELING DATE: 2001-06-04
PRIOR PELING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PALENTIN VUMBER: 60/293,473
PRIOR PELING DATE: 2001-06-25
UNDABER OF SEQ ID NOS: 66
SOFTWARE: PALENTIN VUMBER: 60/293,473
PRIOR PELING DATE: 2001-06-25
UNDABER OF SEQ ID NOS: 66
SOFTWARE: PALENTIN VUMBER: PALENTIN VU
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                                                                                                                                                                340 ACCAGTAGCACTITGTTATTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT
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US-10-039-785-63
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ORGANISM: Artificial sequence
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US-08-958-201-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                  APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 ACCAGTAGCACTTTGTTATTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
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US-10-039-785-54
                                                                                                                                                                    TILLE REPERBACE: PPESO
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-04-05
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-04-05
PRIOR FILING DATE: 2001-11-14
PRIOR PILING DATE: 2001-11-14
PRIOR PILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/331,014
PRIOR FILING DATE: 2001-11-07
PRIOR PRIOR DATE: 2001-11-07
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
Sequence 54, Application US/10039785 Patent No. 6538938
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ORGANISM: Artificial sequence
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 54
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Sequence 13, Application US/08958201 Patent No. 5977319 GENERAL INFORMATION: APPLICANT: Pope, Anthony R

RESULT 11 US-08-958-201-13

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241 CAGGCTGAGGACGAGGCTGATTATTACTGCAGCTCACTTACACGCAGAGTCACTGTGATC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 cchaarcechrordagerceaagrorgedaacacegecroccreacearcrorgedor 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 recrecacresaaceascascasteacerresresrearaacrarererecresraceaeas 120
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Pritchard, Kevin
Williams, Andrew J
Johnson, Kevin S,
VENTION: Specific binding members for estradiol;
VENTION: materials and methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/958,201
FILING DATE:
                                                                                                                                                                                  3: Marshall O'Toole Gerstein Murray & Borun
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .4; DB 2;
3e-72;
ches 36;
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Pred. No. 3e-72
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRICE APPLICATION DATA:
APPLICATION NUMBER: US 60/028,897
FILING DATE: 21-007-1996
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGHH: 333 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 11, Application US/08958201
; Patent No. 2977319
; GENERAL INFORMATION:
APPLICANT: Pope, Anthony R
                                                                                                                                                                                                          STREET: 6300 Sears Tower, 233
CITY: Chicago
STATE: 111inois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER:
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ilarity 89.2%;
Conservative (
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APPLICANT: Pritchard, Kevin
                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 297; Conserv
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RESULT 14
US-10-039-785-60
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Patent No. 6538938
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Attibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
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APPLICANT: Johnson, Kevin S
TITLE OF INVENTION: Specific binding members for estradiol;
TITLE OF INVENTION: materials and methods
NUMBER OF SEQUENCES: 23
CORRESPONDEMEX ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37; Indels
                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/958,201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.2%; Score 273.8; DB 2
88.9%; Pred. No. 8.8e-72;
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                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,897
FILING DATE: 21-0CT-1996
FILING DATE: 21-0CT-1996
FILING CHARACTERISTICS:
LENGTH: 333 base pairs
TYPE: nucleic acid
CTRANDEDNESS: double
                                                                                                                                                                                                              ZIP: 60606-6402
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
MCDUWTTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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IMMEDIATE SOURCE:
CLONE: D12 (light chain)
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                                                                                                                                               CITY: Chicago
STATE: Illinoi
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US-08-958-201-11
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US-10-039-785-57
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Best Local
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280 CTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACA 339
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Patent No. 6538938
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REPERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT PILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60,369,860
PRIOR FILING DATE: 2002-04-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCACCAACTCTTGGGTGTTCGGCGGAGGACCAAGGTCACGTCCTAGGT 735
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Pred. No. 2.2e-70;
0; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: DNA encoding T1014A12 scFv
US-10-039-785-57
PILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT TAPLICATION NUMBER: US/10/039,785
CURRENT FLING DATE: 2002-06-05
PRIOR PILING DATE: 2002-04-05
PRIOR PILING DATE: 2001-12-20
PRIOR PILING DATE: 2001-12-20
PRIOR PILING DATE: 2001-11-14
PRIOR PILING DATE: 2001-11-14
PRIOR PILING DATE: 2001-11-14
PRIOR PILING DATE: 2001-11-14
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-09-21
PRIOR PILING DATE: 2001-09-21
PRIOR PILING DATE: 2001-08-02
PRIOR PILING DATE: 2001-08-02
PRIOR PILING DATE: 2001-08-02
PRIOR PILING DATE: 2001-08-02
PRIOR PILING DATE: 2001-06-04
PRIOR PILING DATE: 2001-06-04
PRIOR PILING DATE: 2001-06-04
PRIOR PILING DATE: 2001-06-04
PRIOR PILING DATE: 2001-06-05
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Best Local Similarity 85.5%;
Matches 300; Conservative
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564 279

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Search completed: December 29, 2003, 21:48:25 Job time: 44.9294 secs
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR APPLICATION NUMBER: 60/349,860
PRIOR PILING DATE: 2002-12-20
PRIOR FILING DATE: 2002-12-20
PRIOR PLING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/31,310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                340 ACCAGTAGCACTTTGTTATTCGGAAGAGGGACCCGGTTGACCGTCTAGGT 390
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Pred. No. 6.6e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.7%; Scor. 85.2%; Pred. No. 0...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: DNA encoding T1014F08 scFv
US-10-039-785-60
PRIOR FILING DATE: 2001-12-20
PRIOR PILING DATE: 2001-12-20
PRIOR PILING DATE: 2001-11-10
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-07
PRIOR PELING DATE: 2001-11-07
PRIOR PELING DATE: 2001-10-09
PRIOR PILING DATE: 2001-00-09
PRIOR PRILING DATE: 2001-00-09
PRIOR PILING DATE: 2001-09-01
PRIOR PELING DATE: 2001-09-02
PRIOR PILING DATE: 2001-09-02
PRIOR PILING DATE: 2001-06-02
PRIOR PILING DATE: 2001-06-02
PRIOR PILING DATE: 2001-06-04
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SOFTWARE: PATENTIN VOS: 66
SOFTWARE: PATENTIN VOS: 66
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Patent No. 6538938
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial sequence
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Best Local Similarity 85.2
Matches 299; Conservative
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US-10-039-785-58
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Pred. No. 5.2e-68;
0; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: DNA encoding T1014B01 scFv
US-10-039-785-58
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-00-09
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR PILING DATE: 2001-06-04
PRIOR PILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 67.0%;
Best Local Similarity 84.0%;
Matches 295; Conservative (
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model	
Run on: December 29, 2003, 16:08:50 ; Search time 1615.57 Sec (without alignments) 9875.644 Million cell upda	7 Seconds updates/sec
Title: US-09-019-441-1 Perfect score: 390 Sequence: 1 ATGGCCTGGACTCTGCTCCTCCCGGTTGACCGTCCTAGGT	AGGT 390
Scoring table: IDENTITY NUC Gapop 10.0, Gapext 1.0	
Searched: 2888711 segs, 20454813386 residues	
Total number of hits satisfying chosen parameters: 5777422	
Minimum DB seg length: 0 Maximum DB seg length: 200000000	
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Database : GenEmbl:*  2	

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

escription	85043 H.sapiens	282 Human	133 H.sapiens	358 H.sapien	035 H.sapi	297 H.sapien	355 H.sapiens	3222	2 H. Sabi	14 H. sapi	50 H.sapi	54 H.sapiens	3102 Homo s	285032 H.Sapiens I	99 H sani	3749 Homo s	1 H.sapiens	5 H.sapien	3 H.sapien	25 H.sapien	Z84919 H.Saplens 1 Z85036 H saniens 1	2 H.sapien	365 Seğu	1 H.sapi	99 H.sapie	7851 Homo	3 5	1760 Homo	17 H.sapien	Э6 Н.	3983 Homo s	24 H.sapien	25 H.sapien	30 H.sapien		n. sapien	76 H 54P	Co H carrier	api
SUMM	HSZ85043	HUMIGLDS	5033	8535	8503	3529	535	AX379222	8536	8503	36	8536	BC033102	HSZ85032	HSU43//Z	BC018749	HSZ85091	HSZ85295	HSZ85303	HSWLRG	HS284919	HSZ85302	AR135365	HSZ85171	HSZ85299	AF417851	HIMICHEDAI.	io	9	529	3098	3492	SZ8492	8503	282	00000	200	202020	HSZ85359
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Ľ	Ξ	Z85303 H.sapiens I	Ξ	Ξ	Ξ	Ξ	AR135365 Sequence	Z85171 H.sapiens I	Z85299 H.sapiens I	AF417851 Homo sapi	X57823 Human rearr	Í	õ	Ξ	Z85296 H.sapiens I	33	Ξ	_	Ξ	Ξ	Ξ	Ë	H.sa	H.Sa	H.sap	
HSZ85091	HSZ85295	HSZ85303	HSWLRG	191	2	HSZ85302	AR135365	HSZ85171	HSZ85299	AF417851	HSIGVL033	HUMIGHEPAL	AY204760	HSZ85197	HSZ85296	8	HSZ84924		HSZ85030	0	HSZ85031	HSZ85300	HSZ84926	36	HSZ85359	
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83.1	82.8	82.8				82.4	82.4					81.9		81.5	81.5	81.5	81.1	81.1	81.1	81.1	81.1	81.1	80.7	80.7	80.7	
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## ALIGNMENTS

HSZ85043 435 bp DNA linear PRI 06-FEB-1997	H.sapiens Ig lambda light (24-17ITIIH34) rearrange	Z85043.1 GI:1834754	antigen receptor; immunogiobulin; immunogiobulin light chain; immunoglobulin superfamily; rearranged; variable region.		Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	1 Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
RESULT 1 HSZ85043 LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE		REFERENCE

REFERENCE AUTHORS

JOURNAL

TITLE

JOURNAL

TITLE

FEATURES

gene

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TCTGCCCCGACTCAGCCTCCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 GCTGAGGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="bears the 8.12 idiotype, which is associated with anti-DNA specificity of SLE autoantibodies; G00-128-432"
Paul.E., Livneh,A., Manheimer-Lory,A. and Diamond,B. Characterization of the human immunoglobulin V-lambda-II gene family and analysis of V-lambda-II and C-lambda polymorphism in systemic lupus erythematosus
J. Immunol. (1991) In press
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1. 473
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Pred. No. 1.4e-85;
0; Mismatches 31
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                                                                                                                                                                                  DS.
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                                                                                                                                                                                                    /db_xref="taxon:9606"
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Best Local Similarity
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Human Ig lambda L chain subgroup II V-2.DS mRNA, VJ region, partial
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 473)
            XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
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          XXX.u.e.
Repertoire
J. Mol. Biol.
E 2 (bases 1 to 435)
AS Ignatovich, O.
Direct Submission
NAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre f
Engineering, Hills Road, Cambridge CB2 2QH, UK
Location/Qualifiers
Location/Qualifiers
A35 ......... sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                  /map="22q11.2"
/clone="44-17TIIH34"
/cell_type="lymphocyte"
/tissue_type="peripheral blood"
/clone_lib="cDNA library"
/rearranged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 340.4; DB 9;
Pred. No. 1.4e-85;
0; Mismatches 31;
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/gene="IGLV"
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92.1%;
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/gene="IGLV"
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Homo sapiens
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M75282.1 GI:186134
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PRI 06-FEB-1997
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270 AATGGTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTGTGGGCTCCAG 329
                                                                             330 GCTGAGGACGAGGACTATTATTACTGCAGCTCATATACAAGCAGCAGCAGCACTTTCGTATTC 389
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ignatovich, O., Tomlinson, I.M., Jones, P.T. and Winter, G. XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
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Submitted (O6-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
Location/Qualifiers
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Pred. No. 4e-85;
0; Mismatches 32;
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/clone_lib="cDNA library"
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/organism="Homo saplens"
/mol_type="genomic DNA"
/isolate="donor IT"
/db_xref="texon:9606"
/map="22q11.2"
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/cell_type="lymphocyte"
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/gene="IGLV"
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Best Local Similarity 91.8%;
Matches 358; Conservative
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2 (bases 1 to 435)
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Human Ig rearranged lambda chain (V-lambda-2.DS) mRNA, V-, J-, and
ברפקוסה subgroup II.
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Paul. B., Livneh, A., Manheimer-Lory, A.J. and Diamond, B.
Characterization of the human Ig V lambda II gene family and analysis of V lambda polymorphism in systemic lupus
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                            C-region; J-region; V-region; immunoglobulin; immunoglobulin lambda; immunoglobulin light chain; variable region subgroup II. Homo sapiens (human)
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fnote="G00-128-432"
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/note="G00-128-432"
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/note="G00-128-432"
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ilarity 92.1%; Pred. No. 1.4e-85;
Conservative 0; Mismatches 31;
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     390 GGCGGAGGACCAAGCTGACCGTCCTAGGT 419
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/gene="IGL@"
/note="leader; G00-128-432"
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/cell type="B lymphocyte"
1. .473
/gene="IGL@"
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/db_xref="taxon:9606"
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/gene="IGL@"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein Engineering, Hills Road, Cambridge CB2 2QH, UK
Location/Qualifiers
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/tissue type="lymphocyte"
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XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (06-FBB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 20H, UK
Location/Qualifiers
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/mol type="genomic DNA"
/mol type="denor SW"
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/map="22q11.2"
/clone="25-288MID60"
/clone="25-288MID60"
/tissue type="peripheral blood"
/clone_lib="cDNA library"
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Pred. No. 3.2e-84;
0; Mismatches 34;
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Submitted (06-FBB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
Location/Qualifiers
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/mol type="genomic DNA"
/isoTate="donor SW"
/mdb xref="texton:9606"
/map="22q1.2"
/clone="25-23SWIB16"
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/tissue_type="peripheral
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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Submitted (06-FBB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
Location/Qualifiers
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Pred. No. 9.1e-84;
0; Mismatches 35; Indels
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/tissue_type="peripheral_blood"
/clone_lib="cDNA_library"
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/isolate="donor Ol at time
/db xref="taxon:9606"
/map="22q11.2"
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Signatovich, C.

Direct Submission

Losubmission

Engineering, Hills Road, Cambridge CB2 20H, UK

Location/Qualifiers

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//mol_type="genomic DNA"
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//db_raref="taxon:9606"
//map="224-12.TTIIE213"
/cell_type="peripheral blood"
/tissue type="peripheral blood"
/cell_type="peripheral blood"
/cell_tissue type="peripheral blood"
/clone_lib="cDNA library"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Compositions and methods for the therapy and diagnosis of colon
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                                    TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC
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Pred. No. 9e-84;
0; Mismatches 35; Indels
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CORIXA CORPORATION (US)
Location/Qualifiers
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Sequence 264 from Patent W00196389.
AX379222
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Best Local Similarity 91.0%;
Matches 355; Conservative (
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06-FEB-1997

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121 TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC 180
241 GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCTG 300
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
Location/Qualifiers
1. 435
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                 antigen receptor; immunoglobulin; immunoglobulin light chain; immunoglobulin superfamily; rearranged; variable region. Homo sapiens (human) Homo sapiens
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H.sapiens Ig lambda light chain variable region gene
(24-08ITIIC194) rearranged; Ig-Light-Lambda; VLambda.
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/isolate="denor IT"
/db_xref="taxon:9606"
/map="2241.2"
/clone="24-08ITIC194"
/call_type="lymphocyte"
/tissue_type="peripheral blood"
/clone_lib="conA library"
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Pred. No. 2.1e-82;
0; Mismatches 38;
                                                                                                                             361 GGCGGAGGGACCAAGCTGACGTCCTAGGT 390
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/gene="IGLV"
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Ignatovich, O.
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 GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTC 360
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 20H, UK
Location/Qualifiers
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84.8%; Score 330.8; DB 9; Length 435;
Best Local Similarity 90.5%; Pred. No. 7.4e-83;
Matches 353; Conservative 0; Mismatches 37; Indels 0
                                                                                                                                                                                                       HS285362 19 lambda light chain variable region gene (25-33SWIIE224) rearranged; Ig-Light-Lambda; VLambda.
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/tissue type="peripheral blood"
/clone lib="cDNA library"
                                                                                            GCGGAGGACCAAGGTGACCGTCCTAGGT 390
                                                                         361 GGAAGAGGACCCGGTTGACCGTCCTAGGT 390
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/mol_type="genomic DNA"
/isolate="donor SW"
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/map="22q11.2"
/clone="25-33SWIIB224"
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Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
Location/Qualifiers
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/mol type="genomic DNA"
/isolate="donor SW"
/db_xref="taxon:9606"
/map="22q11.2"
/clone="25-36SWIF166"
/call type="peripheral blood"
/clone_lib="cDNA library"
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Best Local Similarity 90.3
Matches 352; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ignatovich, 0.
Direct Submission
Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 20H, UK
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antigen receptor; immunoglobulin; immunoglobulin light chain;
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(25-31SWIID182) rearranged; Ig-Light-Lambda; VLambda.
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Pred. No. 2.1e-82;
0; Mismatches 38;
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/clone_lib="cDNA library"
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/isolate="donor_SW"
/db_xref="texon:9606"
/map="22611.2"
/clone="25-31SWIID182"
/cell_type="lymphocyte"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 895)
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Submitted (15-UN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 43 Row: g Column: 22 This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein.
GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG
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/product="Similar to immunoglobulin lambda joining 3"
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Email: cgapbs-r@mall.nih.gov
Tissue Procurement: Louis Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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/clone_lib="NIH MGC_48"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
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BC033102.1 GI:21619847
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/protein_id="AAH33102.1"
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/trānslation="MAWALLLLTLITOGTGSWAQSALTOPPSASGSPGOSUTISCTGT
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DEADYYGSYAYOOFFGTGTKVTVLGOPKANPTVTLFPPSSEELQANGALLVCLIS
DFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQV
THEGSTVEKTVAPTECS"
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                                                                                                                                                                                                                                                                                                                                                                                                                       61 TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 GATCGCTTCTCGCTCCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 ATGGCCTGGGCTCTGCTCCTCCTCCTCCTCCTCAGGGCACAGGGTCCTGGGCCCAG 90
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0
                                                                                                                                                                                                                                         Length 895;
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                                                                                                                                                                                                                                       Score 329.2; DB 9;
Pred. No. 2e-82;
0; Mismatches 38;
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90.3%;
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352; Conservative
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BX280395 BX280395 BI820758 603034354 BG685732 602637827 BG759257 602710936

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Database :

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AV693754 AV693754
AV697043 AV697043
BG756342 602713662
BG756342 602713662
BG756342 60271363
BG756342 602710363
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AV699040 AV699040
AV699040 AV699040
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AV699019 AV699040
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BG785194 6024621
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BG766473 602583943
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AV686421 AV686421
BM831030 K-EST0104
BM831030 K-EST0104
BM831030 K-EST0104
BM831030 K-EST0104
BM831030 K-EST0104
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BM83098 K-EST0104
BM83098 K-EST0104
BM83098 K-EST0104
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602246174F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4337226 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotanika Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 880)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM1211 row. c column: 19
High quality sequence stop: 759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov

Thame Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                   BG397577
BG564971
BG566373
BG754756
AV686421
BM831030
BM769694
BM831125
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BM773502
BM769463
BG541853
BG397282
                                            AV693754
AV697043
BG758901
BG756342
BG756874
BF976229
AW404692
AW404692
AV6994861
AV699040
AV685070
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BG483745
BG342194
BG059377
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Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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BF975970
LOCUS
  CD101742 AGENCOURT
BG756493 602715633
BM914350 AGENCOURT
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                                                                                 December 29, 2003, 16:08:50 ; Search time 1687.58 Seconds (without alignments) 5616.780 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                       1 ATGGCCTGGACTCTGCTCCT......CCCGGTTGACCGTCCTAGGT 390
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             GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                 22781392 segs, 12152238056 residues
                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                        summaries
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CD101742
BG756493
BM914350
                                                           using sw model
                                                                                                                                                                              IDENTITY NUC Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 su
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em_gss_phg:
em_gss_vrl:
gb_gssl:*
gb_gss2:*
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Maximum DB seq length: 2000000000
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em_gss_pln:*
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85.6
85.6
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Score

No. Result

338.8 334 334 334 334

BM830794 K-EST0104 BI823608 603040988 BQ712542 AGENCOURT

BM825633

BM769463 K-EST0052 BG541853 602569746 BG397282 602439065 BG536723 602564852

```
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: NDAM388 row: k column: 08
High quality sequence stop: 585.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1:21 TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGGCCTGGGCTCTCCTCCTCCTCCTCCTCCTCAGGGCACAGGATCCTGGGCTCAG
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Best Local Similarity 91.0%;
Matches 355; Conservative 0
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Homo sapiens
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BG756493
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                                                                                                                                                             /clone="IMAGE:4337226"
/tissue type="brimary B-cells from tonsils (cell line)"
/tissue type="brimary B-cells from tonsils (cell line)"
/lab host="Drimary B-cells from tonsils (cell line)"
/clone lib="MIH MGC 48"
/clone lib="MIH MGC 48"
/clone lib="MIH MGC 48"
/clone lib="Organ: B-cells; Vector: pOTB7; Site l: XhoI;
Site 2: EcoR1; cDNA made by oligo-dT priming.
Site 2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average innert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald W. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 766)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 1.3e-79;
0; Mismatches 32; Indels
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   422
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                                                                           'organism="Homo sapiens"
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                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
             Location/Qualifiers
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Best Local Similarity 91.8%;
Matches 358; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone lib="MIH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site 1: Xho1;
Site 2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1XXho1 sites using the Directionally cloned into EcoR1XXho1 sites using the following 5' adaptor: GGGAGG(G). Size-selected >500bp for average insert size 1:8kb. Library constructed by Ling Hong int the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscribt II RT (Life Technologies).

Note: Library."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can k
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMT705 row: b column: 10
High quality sequence stop: 838.
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Pred. No. 2.4e-78;
0; Mismatches 35;
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.6%;
ilarity 91.0%;
Conservative
                                                                       (bases 1 to 843)
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RESULT 4 BM914350

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1078 bp mRNA linear EST 12-MAR-2002 AGENCOURT 6615290 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480018 5', mRNA Fequence. BM914350 BM914350.1 GI:19364729 EST.
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BCORI; CDNA made by oligo-dT priming. Directionally cloned
into BcoRI/Xho1 sites using the following 5 adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Gtratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library
a 257 c 244 g 150 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATOGOTTOTOTOGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300
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                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   þe
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                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 1078) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished Context Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can bette: Licrobath the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2002 row: d column: 03
High quality sequence stop: 538.
High quality sequence stop: 538.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="texcon:9606"
/lone="IMAGE:5480018"
/lab host="DH108" (phage-resistant)"
/clone_lib="NIH_MGC_113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.6%; Score 334; DB 12;
ilarity 91.0%; Pred. No. 2.7e-78;
Conservative 0; Mismatches 35;
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                                                                                                                                                                                                            Homo sapiens (human)
Homo sapiens
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les 355; Conserv
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us-09-019-441-1.open.rst

VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

DEFINITION

RESULT 5 BX280395

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ACCESSION

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    .787
    /organism="Homo sapiens"

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Homo sapiens
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                     80
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AUTHORS
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JOURNAL
COMMENT
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BI820758
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RI
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1 (bases 1 to 485)
Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelot, U., Schneider, D. and Korn, B.
Human UnigeneSet - RZPD3
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free from RZPD; contact RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>Б</u>С
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Lessue Type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab host="DH10B (ampicillin resistant)"
/clone lib="Scarses multiple sclerosis 2NbHMSP"
/note="Vector: pT73D (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Ex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                             Contact: Ina Rolfs

Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; INAGD998E24628.

RZPD; INAGD99E24628.

RZPDIL18; I.M.A.G. B. CDMA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/Cgi-
bin/showib.pl.cgi/response7libNo-972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="IMAGp998E24628 ; IMAGE:283391"
407 GGCGGAGGGACCAAGCTGACCGTCCTCGGT 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mol_type="mRNA"
db_xref="taxon:9606"
                                                                                                                                                                                     BX280395.1 GI:28613813
                                                                                                                                                                                                                          Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . .485
                                                                                                                                                                                                                                           Homo sapiens
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Best Local S
Matches 353
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source

FEATURES

61 TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120

BASE COUNT ORIGIN

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/MOL type="mRNA"
// Ab xref="taxon:9606"
// Clone="INAGE:175684"
// lab host="MAGE:175684"
// lab host="D4108"
// clone=lib="NIH MGC 115"
// clone=lib="NIH MGC 115"
// note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: Not!; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69: Library is
oligo-AT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1:8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Inviriogen). Research Genetics tracking code
021. Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BI820758 787 bp mRNA linear EST 04-OCT-2001
                                                                                                                                                                                                                                               240
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                                                                                                                                                                                                                                                                                     200 CCAGGCAAAGCCCCCAAACTCATGATTTATGAGGTCAGTAAGCGGCCCTCAGGGGTCCCT 259
                                                                                                                                                                                                                                                                                                                                                                                 GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                       260 GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGGCTCCAG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

http://image.llnl.gov k column: 13

High quality sequence start: 2

High quality sequence stop: 785.
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I (bases 1 to 787)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                                                                                                                                                                                                           181 CCAGGCAAAGCCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 GGAAGAGGACCCGGTTGACCGTCCTAGGT 390
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686 bp mRNA linear EST 15-MAY-2001
602710936F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851128 5',
mRNA sequence.
BG759257
EG759257.1 GI:14069910
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   for average insert size 1.8kb. Library constructed by Li Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis Kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.h column: 09
High quality sequence stop: 683.
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Pred. No. 1.7e-77;
0; Mismatches 37;
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/db_xref="taxon:9606"
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Best Local Similarity 90.5%;
Matches 353; Conservative
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NIH-MGC http://mgc.nci.nih.gov/.
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/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 48"
/note="Organ: B-cells, Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; coDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Libra at:
http://image.llnl.gov
Plate: LicMi624 row: f column: 08
High quality sequence stop: 821.
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                Length 787;
             Score 330.8; DB 12; Length
Pred. No. 1.7e-77;
0; Mismatches 37; Indels
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/db_xref="taxon:9606"
/clone="IMAGE:4765447"
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90.5%;
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AV697043 AV697043 GKC Homo sapiens cDNA clone GKCGWG01 5', mRNA sequence. AV697043
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1 (bases 1 to 767)

Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.

Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
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                                                                                                                                                                                                                                                                                                                        /clone_lib="GKC"
/note="Vector: pBluescript_sk(-); Site_l: EcoRI; Site_2:
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China 141: 86-21-50801919(ex. 45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.ch
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGCCTGGGCTCTGCTATTCCTCACCCTCCTCACTCAGGGCACAGGGTCCTGGGCCCAG
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                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mkNa"
/db xref="taxon:966"
/clone="GKCGWD05"
/tissus type="hepatocellular carcinoma"
/dev stage="Adult"
/lab_host="SQLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 329.2; DB 9;
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0; Mismatches 38
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Best Local Similarity 90.3%;
Matches 352; Conservative (
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                     /tissue_type="primary B-cells from tonsils (cell line)"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 48"
/clone lib="NIH MGC 48"
/note="Organ: B-cells, Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI; cDNA made by.oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAGG(G). Size-selected 550bb for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
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I bases 1 to 716)

Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, M., Shen, X., Lud, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.

Insight into hepatocellular carcinogenesis at transcriptome level
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Chinese National Human Genome Center at Shanghai
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                                                                                                                                                                                                                                                                                                                                               84.4%; Score 329.2; DB 190.3%; Pred. No. 4.3e-77; ive 0; Mismatches 38
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 786)
NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88
                                                                                                                                                                                                                                                                                                        /clone_lib="GKC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
21625106
11752456
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
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                                                                                                                                                                                                                                                        // tissue_type="hepatocellular carcinoma"
// dev_stage="Adult"
// lab_host="SOLR"
                                                                                                                                                    This clone is available at CHGC in Shanghai
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             Score 329.2; DB 9;
Pred. No. 4.5e-77;
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                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKCGWG01"
                                                                                                                                                                                                                                                                                                                                                  198 g
                                                                                                         Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
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602713662F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853919 5', BG756342
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                                                                                                                                               cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1699 row: i column: 03
High quality sequence stop: 786.

1. 786
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 4.5e-77
0; Mismatches 38
                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 t
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Best Local Similarity 90.3%;
Matches 352; Conservative
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/organism="Homo sapiens"
//organism="Homo sapiens"
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//db_xref="txxnn:9606"
//done="rxnnser:4850871"
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//lab_host="brimary B-cells from tonsils (cell line)"
//lab_host="min MidG 48"
//clone lib="min MidG 68"
//clone lib="min"
//clone 
                                                                                                         BG756874 1inear EST 15-MAY-2001
602710363F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4850871 5',
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Bukaryogia.

Bukaryogia.

Mammalia: Butheria: Primates; Catarrhini; Hominidae; Homo.

Mammalia: Butheria: Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 9018)

NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Clone distribution: MGC clone distribution information can be
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1692 row: m column: 16
High quality sequence stop: 885.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.4%; Score 329.2; DB 1
90.3%; Pred. No. 4.8e-77;
iive 0, Mismatches 38
                                                                                                                                                                                                    BG756874.1 GI:14067527
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Best Local Similarity 90.33
Matches 352; Conservative
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VERSION
KEYWORDS
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ORGANISM
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ORIGIN
                                                                                                                                         DEFINITION
                                                          RESULT 13
BG756874
LOCUS
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AUTHORS
TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 48"
/note="Organ: B-cells, Vector: pOTB7; Site_1: Xhol;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/Xhol sites using the following 5' adaptor: GGACGAGG(6). Size-selected s500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: Capbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1700 row: 1 column: 16
High quality sequence stop: 810.
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                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 889)
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                                                                                                                                                                                                 NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
/clone="IMAGE:4853919"
        BG756342.1 GI:14066995
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al Similarity 90.3%;
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/iissue_type="primary B-cells from tonsils (cell line)"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5: adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M: Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Supersoript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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602439086F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4565516 5',
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1282 row: k column: 21
High quality sequence stop: 881.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 980)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
/clone="IMAGE:4565516"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NH1MGC_48"
/clone_lib="NH1MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXXhol sites using the
following 5' adaptor: GGGAGGGG, Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: Lib: sis a NIH MGC Library."
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: WGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1208 row: h column: 02
High quality sequence stop: 777.
High quality sequence stop: 777.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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90.3%; Pred. No. 4.9e-77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:4336177"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 953)
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TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
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LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
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ò	61 TCTGCCCCGACTCCCTCCTCTGTGTCTCTGGACAGTCGGTCACCTCC 120
Ωp	93 TCTGCCCTGACTCAGCCTCCCCTCGGGTCTCCTGGACAGTCAGT
ò	121 IGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC 180
QQ	153 TGCACTGGAACCAGCAGTGATTATTATAACTATGTCTCCTGGTACCAACAGCAC 212
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q	273 GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGGCTCCAG 332
ò	301 GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTC 360
ДQ	333 GCTGCGGATGAGGCTGATTATTACTGCAGCTCATATGCAGGCAG
ò	361 GGAAGAGCGGTTGACCGTCCTAGGT 390
qq	393 GGGGAGGACCAAGCTGACGTCCTAGGT 422

Search completed: December 29, 2003, 21:44:05 Job time : 1691.58 secs

Sequence Sequence Sequence Sequence ( Sequence 18093, A Sequence 18093, A Sequence 15053, A Sequence 57, Appl

Sequence Sequence Sequence

Sequence Sequence

Sequence Sequence

Sequence Sequence Sequence

Sequence

ALIGNMENTS

64, Appl 4, Appli 1654, A 54, Appl 54, Appl

Sequence

Sequence Sequence Sequence Sequence Sequence S

US-10-198-053-267
US-09-918-955-16199
US-09-191-353-146
US-10-139-785-69
US-10-139-785-64
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US-10-029-386-15053
US-10-029-386-15053
US-10-039-785-57
US-10-039-785-60
US-10-032-673-63

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KLOETZER, William S.
NAKAMURA, Takehiko
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
ANTIBODIES AND USE THEREOF AS THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Alexandria

CITY: Alexandria

STATE: Virginia

COMPUTRY: United States

ZIP: 22313-1404

COMPUTR: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTR: IBM PC COMPATIBLE

COMPUTR: IBM PC COMPATIBLE

COMPATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Ver

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/019,441

FILING DATE: 05-Feb-1998

CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09019441 Publication No. US20030086921A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: REFF, Mitchell E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 836.
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
269
267.8
267.8
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269.4
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264.6
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Sequence 13540, A
Sequence 36573, A
Sequence 16692, A
Sequence 8, Appli
Sequence 13, Appli
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Sequence 13, Appl
Sequence 13540, A
Sequence 15500, A
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Sequence 1, Appli
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76, Appl
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Sequence 73, Ap
Sequence 76, Ap
Sequence 267, Ap
Sequence 267, Ap
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                                                                                                                                            ; Search time 563.449 Seconds
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1 ATGGCCTGGACTCTGCTCCT......CCCGGTTGACCGTCCTAGGT 390
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-103-686-1
US-10-198-846-13206
US-10-198-846-13540
US-09-918-995-16692
US-10-076-747-8
US-10-225-108A-13
US-10-198-846-13540
US-10-158-646-76
US-10-158-646-76
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US-09-907-969-267
US-09-827-271-267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                         December 29, 2003, 19:01:43
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Maximum Match 100%
Listing first 45 summaries
                                                                                                   nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Match Length DB
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Version #1.30

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RPDLICANT: REFF, William S.

NAKAMURA, Takehiko.

TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
ANTIBODIES AND USE THEREOF AS THERADEUTICS
                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                     Length 390;
                                                                                                                                                                                                                                                                                   0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSES: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: Alexandria
                                                                                                                                                                                                                                                   100.0%; Score 390; DB 11;
100.0%; Pred. No. 6.1e-118;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/103,686
                                                                                                                                                                                 LOCATION: 58. 390
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10103686; Publication No. US20030059424A1; GENERAL INFORMATION:
                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
          LENGTH: 390 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                 NAME/KEY: mat_peptide
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 35
                                                                                                                                 1..390
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 390; Conservative
                                                                                                                 NAME/KEY:
                                                                                                                                 LOCATION:
                                                                                                                                                 FEATURE:
                                                                                                FEATURE
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US-10-103-686-1
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61 TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCCTGGACCAGTCGGTCACCATCTCC 120
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Publication No. US200309974A1
Publication No. US200309974A1
APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Steinman, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OP INVENTION: THERAPY OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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100.0%; Pred. No. 6.1e-118;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                  MAME: TESKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAAGAGGACCCGGTTGACCGTCCTAGGT 390
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                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-103-686-1
FILING DATE: 25-Mar-2002
CLASSIFICATION: <Unknown>
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58..390
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.0
Matches 390; Conservative
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                                            2 TGGCCTGGACTCTGCTCCTCGTCACCTCACTCAGGCCACAGGATCCTGGGCTCAGT
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; bedication No. US20030073623A1
; GENERAL INFORMATION:
APPLICANT: Hyseq. Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT FILICATION NUMBER: US/09/918,995
CURRENT FILIGE DATE: 2001-07-30
; PRIOR PRIICATION NUMBER: US/09/235,076
; RICH RELICATION NUMBER: US/09/235,076
; ROUTWARE: FABELSEQ for Windows Version 3.0
; SOFTWARE: FabelseQ for Windows Version 3.0
; LENGTH: 408
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Pred. No. 2.3e-96;
0; Mismatches 41
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Best Local Similarity 89.5%;
Matches 349; Conservative
    350; Conservative
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US-09-918-995-36573
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; Publication No. US203009974A1
; Publication No. US203009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Lillie, James
; APPLICANT: Wang, Youzhen
; APPLICANT: Wang, Youzhen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FASELSEQ for Windows Version 4.0
; SEQ ID NO 13540
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84.0%; Score 327.6; DB 15; Length
Best Local Similarity 90.0%; Pred. No. 3.3e-97;
Matches 351; Conservative 0; Mismatches 39; Indels
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Pred. No. 7e-97;
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FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
FRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FBSESEQ for Windows Version 4.0
SEQ ID NO 13206
LENGTH: 1640
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90.0%;
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Best Local Similarity
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; ORGANISM: Homo E
US-10-198-846-13206
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US-10-225-108A-13
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259 AATGGCTTCTGGGTTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 318
                                                   GCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTATTC 360
                                                                        319 GCTGAGGACGAGGCTCATTATTATTGCAGTTCATATACAACCAGAAGCACTCTCGTCTTC 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
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                                                                                                                                                                                                                                  Sequence 16692, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: FROW VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: FROW VARIOUS CDNA LIBRARIES
TILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/235,076
PRIOR PILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.2%; Score 324.4; DB 1
89.5%; Pred. No. 2.3e-96;
iive 0; Mismatches 41
                                                                                                                    361 GGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
                                                                                                                                          379 GGAAATGGGGCCAAGGTCACCGTCCTATGT 408
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16692
LENGTH: 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 89.5
Matches 349; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-16692
                                                                                                                                                                                                         RESULT 6
US-09-918-995-16692
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Sequence 8, Application US/10076747
Publication No. US20030180726A1
GENERAL INFORMATION:
APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto

US-10-076-747-8

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APPLICANT: Karra, Kabana
APPLICANT: Karra, Kabana
APPLICANT: Sun, Yongming
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Ovarian Specific Genes and P)
FILE REFERENCE: D8X-0315
CURRENT APPLICATION NUMBER: US/10/076,747
CURRENT PILING DATE: 2002-02-13
PRIOR FILING DATE: 2001-02-13
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CACTGGAACCAGCAGTCACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAGCACCC 180
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Publication No. US20030157112A1

GENERAL INFORMATION:
APPLICANT: HOOPER, Craig

APPLICANT: DIETZSCHOLD, Bernhard
ITILE OF INVENTION: Recombinant Antibodies, and Compositions
TITLE OF INVENTION: and Methods for Making Them
FILE REPERBUCE: 93121-110

CURRENT APPLICATION NUMBER: US/10/225,108A

CURRENT FILING DATE: 2003-04-10

PRIOR APPLICATION NUMBER: US 09/848,832

PRIOR FILING DATE: 2001-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41; Indels
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Pred. No. 1.6e-95;
0; Mismatches 41;
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Best Local Similarity 89.4%;
Matches 347; Conservative
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LOCATION: (1022)..(1022)
OTHER INFORMATION: a, c, g
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ORGANISM: Homo sapien
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US-09-918-995-16500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTGAGGATGAGGCTGATTATTACTGCTGCTCATATGCAGGCGACTACACCCCGGGCGTG 375
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PREVENTION, AND
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                                                                                                                                                                                                                                                                                                                                              Length 726;
                                                                                                                                                                                                                                                                                                                                              Score 313.2; DB 13; Length
Pred. No. 1.4e-92;
0; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 135-0.7

Publication No. US2003009974A1

GENERAL INPORMATION:

APPLICANT: Xu, Yongyao

APPLICANT: Xu, Yongyao

APPLICANT: Wang, Youthen

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: THERAPY OF BREAST CANCER

FILE REFERENCE: MRI-049

CURRENT FAPLICATION NUMBER: 60/306,220

PRIOR APPLICATION NUMBER: 60/306,220

PRIOR FILING DATE: 2002-07-18

PRIOR FILING DATE: 2011-07-18

NUMBER OF SEQ ID NOS: 14004

SEG ID NOS: 14004

LEMANTAL: 1507

SEG ID NOS: 14004

LEMANTAL: 1507

SEG ID NOS: 14004

LEMANTAL: 1507
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88.9%; Pred. No. 1.8e-92;
ive 0; Mismatches 38;
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PRIOR APPLICATION NUMBER: C. ...
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: US 60/314,023
PRIOR FILING DATE: 2001-08-21
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 736
                                                                                                                                                                                                                                                                                                                                                 88.9%;
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Matches 352, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 80.3
Best Local Similarity 88.5
Matches 352; Conservative
                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-198-846-13540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
US-10-198-846-13540
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Pred. No. 3.8e-92;
0; Mismatches 49; Indels 0;
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; Sequence 16500, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INPORMATION:
    APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
; FILE REPERBNCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 1999-01-20
; PRIOR PILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: PRESECTED (FILING WINGOWS VERSION 3.0
; SEQ ID NO 16500
; LENGTH: 420
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Best Local Similarity 87.4%;
Matches 341; Conservative 0
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265 AATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGGCTCCAG 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030073105A1 1329913.2
US-10-158-646-73
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Sequence 73, Application US/10158646
Publication No. US20030073105A1
GENERAL INPORMATION:
APPLICANT: Lasek, Amy K.W.
TITLE OF INVENTYON: CENES EXPRESSED IN COLON CANCER
FILE REFERENCE: PA-0030-1 US
CURRENT APPLICATION NUMBER: US/10/158,646
CURRENT FILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PERL PROGRAM
SEQ ID NOS: 78
LENGTH: 983
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US-10-158-646-73
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RESULT 12
US-10-158-646-76/C
'Sequence 76, Application US/10158646
'Publication No. US20030073105A1
'GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE THERAPY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc feature
; OTHER INFORMATĪON: Incyte ID No. US20030073105A1 1329881.6
US-10-158-646-76
APPLICANT: SOTNESSE, Thierry
TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
TITLE REPERENCE: PA-0030-1 US
CURRENT APPLICATION NUMBER: US/10/158,646
CURRENT PILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: 60/295,239
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PERL PROGRAM
SEQ ID NO 76
LENGTH: 2667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 267, Application US/0988441
; Sequence 267, Application US/0988441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
    APPLICANT: Adgate, Paul A.; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER; FILE REFERENCE: 210121.4627.
; CURRENT PELLIATION NUMBER: US/09/884,441
; CURRENT FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2275 TGGCGGAGGGACCAAGTTGACCGTCCTAGGT 2245
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NAME/KEY: misc_feature
LOCATION: (1)...(548)
                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapien
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121 TGCACTGGAACCAGGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC 180
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1 ATGGCCTGGACTCTGCTCGTCACCCTCCTCACTCAGGGCACAGGATCCTGGGCTCAG
                                                                           TCTGCCCCGACTCAGCCTCCCTCTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC
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; Publication No. US20030165504A1
; Publication No. US20030165504A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER;
; FILE REFERENCE: 210121.46226
; CURRENT PAPLICATION NUMBER: US/09/827,271
; CURRENT PILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 461
; SEQ ID NO 267
; LENGTH: 548
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; LOCATION: (1)...(548)
; OTHER INFORMATION: n = A,T,C or G
US-09-827-271-267
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ORGANISM: Homo sapien
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JAPPLICANT: Mindicham, Jennifer L.
APPLICANT: King, Gordon E.
JAPPLICANT: Algate, Paul A.
APPLICANT: Filing, Steven P.
APPLICANT: Fering, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Red, Steven G.
APPLICANT: Red, Steven G.
APPLICANT: Red, Steven G.
APPLICANT: Red, Steven G.
APPLICANT: Albone, Earl
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF OVARIAN CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.4228
CURRENT FILING DATE: 201-07-17
NUMBER OF SEQ ID NOS: 596
SOFTWARE: FASISEQ for Windows Version 4.0
                                                             Length 548;
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                                                                                                46; Indels
                                                       Score 295.2; DB 10;
Pred. No. 1e-86;
0; Mismatches 46;
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; Publication No. US20030091580A1
; GENERAL INFORMATION:
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1 LOCATION: 346, 358, 432, 510, 512

2 OTHER INFORMATION: n = A,T,C or G

US-09-907-969-267
    or
                                                         Query Match 75.7%;
Best Local Similarity 87.7%;
Matches 343; Conservative
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  OTHER INFORMATION: n
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US-09-907-969-267
    ; OTHER INFURM
US-09-884-441-267
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Mouse DNA encoding DNA encoding throm DNA encoding novel Human prostate exp Human prostate exp

DNA encoding novel

Human ovarian carc Ovarian carcinoma

Human prostate exp Human prostate exp Human autoantibody Nucleotide sequenc Nucleotide sequenc MH4H7 MAD light ch Variable region of

DNA encoding anti Nucleotide sequenc Nucleotide sequenc Human U266 lambda

U266-Lambda gene a

Human autoantibody APRIL binding scFv Recombinant human

Recombinant

Post-processing:

Database

Minimum I Maximum I

Perfect score:

Sequence:

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Scoring table:

DNA encoding singl
DNA encoding throm
DNA encoding singl
DNA encoding throm
Mouse DNA encoding
Thrombopoietin (TP

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Anti-human CD23 6G5 monoclonal antibody light chain variable region DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-human CD23 6GS monoclonal antibody; light chain variable region; human CD23; IgG; FCeRii/CD23; gamma-1 constant region; gamma-3 constant region; allergy; inflammation; autoimmune disease; allergic rhintis; conjunctivitis; autoimmune haemolytic anaemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "anti-human CD23 6G5 light chain variable
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/note= "encodes CDR 1 region"
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ABK43226
AAH42401
AAH42407
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AAQ23370
ABX00205
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ABN72851
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ABV28405
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ABV77130
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AAQ36134
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1.390
/*tag= a
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(first entry)
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  Macaca fascicularis
misc_feature
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Antibody D lambda
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Colon adenocarcino
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DNA encoding novel
DNA encoding monoc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | SIDSI/goddata/geneseq/geneseqn-embl/NA1981.DAT:
| SIDSI/goddata/geneseqy-embl/NA1981.DAT:
| SIDSI/goddata/geneseqy-embl/NA1981.DAT:
| SIDSI/goddata/geneseqy-embl/NA1981.DAT:
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| SIDSI/goddata/geneseqy-embl/NA1985.DAT:
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1 ATGGCCTGGACTCTGCTCCT......CCCGGTTGACCGTCCTAGGT 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Geneseq 19Jun03:*
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.
                         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                   2552756 segs, 1349719017 residues
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                                                                                                                                                      December 29, 2003, 16:08:50
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Maximum Match 100%
Listing first 45 summaries
                                                                                                               nucleic search, using sw model
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AAQ35100
AAS77073
AAS83480
ABX12863
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Gapop 10.0 , Gapext 1.0
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DB seq length: 200000000
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Match Length DB
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322.4 321.2 319.6 316.4 313.6

Score

Result

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WPI; 2002-098052/13.
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Best Local Similarity
Matches 355; Conserv
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                                                                                                           23-APR-2002
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        361
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                                         RESULT 2
ABK29738
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                                                                                                                                                                                                                                                                                                                                 The present sequence represents a DNA sequence encoding the light chain variable region of primate monoclonal antibody anti-human CD23 6G5. The invention provides primate monoclonal antibodies which specifically bind human CD23, the low affinity receptor for IgE (FCeRij(CD23), and comprise either of a human gamma-1 or human gamma-3 constant region that binds to human FC gamma receptors and inhibits IgE expression. The monoclonal antibodies of the invention are claimed to be useful for inhibiting induced IgE production for treating or preventing allergic, inflammatory and autoimmune conditions e.g. allergic rhinitis conjunctivitis, autoimmune haemolytic anamia, etc.
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                                                                                                                                                                                                                                                                    New anti-human CD23 monoclonal antibody - used for inhibiting IgE expression to treat or prevent allergic, inflammatory and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 390; DB 19; Length 390; 100.0%; Pred. No. 1.7e-109; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 390 BP; 74 A; 123 C; 96 G; 97 T; 0 other;
          /*tag= e
/note= "encodes CDR 2 region"
328..357
                                           /*tag= f
/note= "encodes CDR 3 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Updated on 25-MAR-2003 to correct PR field.)
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                                                                                                                                                                                                              Reff MB;
                                                                                                                                             97US-0803085.
98US-0019441.
                                                                                                                        98WO-US02253
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211..231
                                                                                                                                                                             PHARM CORP.
                                                                                                                                                                                                                                                                                           auto:immune conditions
                                                                                                                                                                            (IDEC-) IDEC PHARM COR:
(SEGK ) SEIKAGAKU CORP
                                                                                                                                                                                                                                    WPI; 1998-467495/40.
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Best Local Similarity
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misc_feature
                                 misc_feature
                                                                                                                                             20-FEB-1997;
05-FEB-1998;
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The invention relates to an isolated polynucleotide (I) encoding a polypeptide (II) comprising a portion of a colon tumour protein. A new colsympeptide (III) that bybridises to (I) is useful for determining the presence of a cancer in a patient. (II) or antigen presenting calls specific for a tumour protein, by contacting T cells expecific for a tumour protein, by contacting T cells expecific for a tumour protein, by contacting T cells (II). (II) or antigen presenting calls that express (II) are useful for treating cor antigen presenting cells that express (II). (II), or antigen presenting cells that express (II) are useful for treating to antigen present that calls proliferate, and administering to the patient and from a patient by incubating CD4+ and/or CD8+ T cells isolated (II), so that T cells proliferated T cells, thus inhibiting the ceffective amount of the proliferated T cells, thus inhibiting the ceffective amount of the patient. A new composition is useful in vaccines and paramaceutical compositions for prevention and treatment of stimulating an immune response in a patient. (I) or (II) is useful in vaccines and paramaceutical compositions for prevention and treatment of colon cancer and for the diagnosis and monitoring of the cancers. (I), (II) or an antibody against (II) is useful as a probe or primer for or therapy of human colon cancer. (I) is useful as a probe or primer for molecules for inhibiting expression of (II) in tumour cells. ABX29475-ABX29851 represent human colon adenocarcinoma-specific cDNA sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TCTGCCCCGACTCAGCCTCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGGCCTGGACTCTGCTCCTCGTCACCTCACTCAGGGCACAGGATCCTGGGCTCAG
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Pred. No. 2.9e-92;
0; Mismatches 35; Indels (
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GGAAGAGGACCCGGTTGACCGTCCTAGGT 390
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ilarity 91.0%;
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22-NOV-2000; 2000US-252614P.
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WPI; 2001-030926/04.
P-PSDB; AAB63212.
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TCTGCCCTGACTCAGCCTGCCTCCTGGTCTGGGTCTCCTGGACAGTCGACCATCTCC 152
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                                                                                                                                AATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAA 332
                                                                                                                                                                           GCTGAGGACGAGGCTGATTATTACTGCAGCTCATATACTAGCATCATCACTGTGGTATTC 392
                                                                                                                     241 GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300
                                                                                                                                                              GCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTATTC 360
                                              CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT
                                                                                                                                                                                                                                                                                                                                                                     Human, gene, 88; ovarian specific nucleic acid; OSNA, ovarian cancer, non-cancerous ovarian disease; gene therapy; vaccine; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated OSNA nucleic acid and encoded polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating ovarian cancer and non-cancerous diseases in ovarian tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cafferkey R;
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                                                                                                                                                                                                                                                                                                                                                 Human ovarian specific nucleic acid DEX0310_8.
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15-FEB-2001; 2001US-268834P.
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      a method for determining the presence of an ovary specific protein in a sample and a vaccine comprising an OSP or OSNA. The methods and compositions of the present invention are useful for identifying, diagnosing, monitoring, staging, imaging and treating ovarian cancer non-cancerous disease in ovary tissue. The present sequence is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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specific protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 322.4; DB 29
Pred. No. 1.5e-88;
0; Mismatches 41
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Best Local Similarity 89.4%;
Matches 347; Conservative
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                                                                 The present invention provides the coding and protein sequences for a number of human immune system associated proteins (HISAPS). These can be used in the diagnosis and treatment of various autoimmune disorders, infections and cell proliferation diseases. The diseases include AIDS, adult respiratory distress syndrome, anaemia, asthma, atherosclerosis, crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus, arterlosclerosis, cirrhosis and cancer.
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New human immune system associated proteins (HISAP) and polynucleotides encoding the HISAP, useful for diagnosing, treating or preventing immune or cell proliferative disorders or infections
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                                                                                                                                                                                             DB 22; Length 891;
                                                                                                                                                                                                                  43; Indels
                                                                                                                                                                      Sequence 891 BP; 207 A; 287 C; 222 G; 175 T; 0 other;
                                                                                                                                                                                           82.4%; Score 321.2; DB 2
89.0%; Pred. No. 2.8e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAAGAGGACCCGGTTGACCGTCCTAGGT 390
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                                              Claim 3; Column 87-90; 54pp; English
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Matches 347; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequences given in AAQ35099-100 encode the heavy and light chains of Antibody D respectively. Antibody D is a monoclonal antibody which was derived from peripheral blood lymphocytes from a hepatitis A virus (HAV) sero positive patient. Antibody D is closely related in nature to murine antibody BSB3. Total RNA was isolated from antibody D expressing cells and polyadenylated RNA was extracted. These polyA RNA's were used to prepare a cDNA library which was screened for human kappa light (L) chains and two positive clones were detected. Further heavy (H) chain clones were also isolated. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGGCCTGGGCTCTGCTGCTCCTCACCCTCCTCAGGACACAGGGTCCTGGGCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 902 BP; 225 A; 285 C; 218 G; 174 T; 0 other;
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Matches 346; Conservative
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23-MAR-1992;
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disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic formet directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC
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                                                                                                                                                                                                                                                                                                                            81.1%; Score 316.4; DB 2.88.2%; Pred. No. 8.3e-87; iive 0; Mismatches 46
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Matches 344; Conservative
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medical imaging; diagnostic; genetic disorder;
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(first entry)

10-MAY-2003

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving contrictating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disourcers in the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in the polypeptide for generic disorders for other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human ocid sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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89.1%; Pred. No. 5.7e-86;
ive 0; Mismatches 39; Indels
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Matches 351; Conservative
                                                                                                                 2001-639362/73
Liu C,
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ABX12863 standard; DNA; 726

RESULT 8 ABX12863 ۵×

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The invention discloses a recombinant antibody comprising a constant region of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable region. Rabies is an acute, nearfolgical disease caused by infection of the creatural nervous system with the rabies virus, a member of the Lyssavirus genus of the family Rhabdoviridae. Also disclosed are methods for producing an isolated recombinant antibody by culturing a host cell, containing a recombinant expression vector comprising the mucleic acid molecule encoding the antibody, and isolating the recombinant antibody administering to the individual exposed to a pathogen by administering to the individual the recombinant antibody. The recombinant antibodies are useful for preventing (vaccine) and treating an individual for the qualitative and quantitative determination of the rabies virus. The generoes presented are the antibody protein fragments, the nucleic acids encoding them or the PCR primers used to construct the recombinant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant antibody comprising a constant region of Mab 57 linked to a non-Mab 57 variable region, useful for treating an individual exposed to a pathogen, e.g. rabies infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 ATGGCCTGGGCTCTGCTCCTCCTCAGCCTCCTCAGGGCACAGGATCCTGGGCTCAG
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                                                                                                Human, gene, ds; antibody, constant region, monoclonal antibody 57; Mab 57; variable region; Rabies; neurological disease; infection; central nervous system; rabies virus; Lyssavirus; Rhabdoviridae; pathogen; vaccine; virucide; light chain.
                                                                   monoclonal rabies virus antibody light chain, clone 57
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Sequence 448 BP; 89 A; 142 C; 113 G; 104 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, colypeptide (II) sequences. (I) is useful as hybridisation probes, colypemers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques contour contour and activity of (II) or to treat disease states involving contour and activity of (II) or to treat disease states involving contour and protein as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical contour and paperant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in capanostics, forensics, gene mapping, identification of mutations contour contour contours and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human contour co
                  GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 315
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                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                            DNA encoding novel human diagnostic protein #12874
                                                                                                                               TTATTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
                                                                                                                                                  376 GTTTTCGGCGGAGGACCAAGCTGACCGTCCTAGGT 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 12874; 103pp; English.
                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                              AAS77070 standard; cDNA; 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-639362/73.
P-PSDB; ABG12883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biodiversity
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                              256
                                                                                               316
                                                                                                                                                                                                                                                                             AAS77070;
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                                                                                                                                                                                                                             AAS77070
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                                                                                                                                                                                                                                                                                    167
                                                                                                                                                                                                                                                                                                                                                                                                     227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGAGGACGAGGCTGATTATTACTGCTGCTGATATGCAGGTAGTAGTAGCACTTATGTTC 407
                                                                                                                                                                      48 ATGGCCTGGGCTCTGCTCCTCACTCTCTCACTCAGGACACAGGGTCCTGGGCCCAG 107
                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for treating autoimmune diseases (e.g. rheumatoid arthritis)
                                                                                                                                                                                                                                                                                          TCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCC
                                                                                                                                                                                                                                                                                                                                                                                                     recacregaaccaecagreargringaaarraraaccrrercrecregraccaacaecac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAGGCAAAGCCCCCAAACTCATAATTTATGAGGCAGTAAGCGCCCCTCAGGAGTTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               288 AGTCGCTTCTCTGGCTCCAAGTCTGGCAACACGCCTCCCTGACAATGTCTGGGCTCCAG
                                                                                                                                                                                                                                  TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC
                                                                                                                                                                                                                                                                                                                                                TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAGGCAAAGCCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGCCTCAGGGGTCTCT
                                                                                                                 1 ATGGCCTGGACTCTGCTCCTCGTCACCCTCACTCAGGGCACAGGATCCTGGGCTCAG
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Flt-3 ligand; Fms-like tyrosine kinase; mouse; human; vaccine; immunotherapy; therapy; tumour; lymphoma; gene therapy; VR1642; plasmid VAXID; antibody; idiotype; vector; ss.
                                                           ö
79.5%; Score 310; DB 23; Length 448; 87.2%; Pred. No. 5.9e-85;
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGAAGAGGACCCGGTTGACCGTCCTAGGT 390
                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGACCTGGGACCAAGGTCACCGTCCTAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bicistronic idiotype plasmid VR1642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF30316 standard; cDNA; 7528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - Cytomegalovirus.
- Mus musculus.
- Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JUL-2000; 2000WO-US20679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0146170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-123319/13.
                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INC
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Tsunoda H;

Yabuta N,

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The invention relates to a new modified single chain FV antibody containing at least two Heavy chain variable domains and at least two light chain variable domains from the same or different monoclonal antibodies and which is an agonist for errosslinking a molecule at the cell surface or within the cell and thereby transducing a signal into the cell. Also include are the DNA encoding the antibody, animal cells and microorganisms transformed by and expressing the DNA, the preparation of the antibodies by culture of the transformed cells, drug compositions containing the antibodies and an assay method for the agonist activity of the antibodies by contacting the antibodies with cells expressing the relevant cell surface or internal molecule. The antibodies are useful for treatment and prevention of cancer, inflammatory disease, hormonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 AATGGTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGAGGACGAGGCTGATTATTACTGTTGTTATACAACCAGTAGCACTTTGTTATTC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATGTGCTGACTCAGCCACCCTCGGTGTCAGGGTCTCCTGGACAGTCGATCACCATCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ariesceries Activitation de la contraction de la 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 recacregaaccagcagreactregregrianaacrarercrecregraccaacac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ccaescaaasccccaaacrcarsarrrarsassescasraaacesccrcassesrrrcr
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                                                                                                                                                                                                                                                                                                                                                                                                                             Modified single chain multimeric Fv antibody acting as a signal transduction agonist for treatment of inflammatory hormonal and blood disorders and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGCCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence encoding an antibody of the invention or a fragment thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders including diabetes, autoimmune disease, leukaemia, dysendocrinism and blood disorders. The present sequence is a DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.7%; Score 307; DB 24; Length 387; Larity 87.1%; Pred. No. 4.6e-84; Conservative 0; Mismatches 50; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 387 BP; 79 A; 124 C; 95 G; 89 T; 0 other;
                                                                                                                                                                                                                                                                Ohtomo T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 8; Page 205-206; 217pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           387
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                                                                                                                                                                                                                                                                    Uno S,
       20-OCT-2000; 2000ur-0222-
12-MAR-2001; 2001WO-JP01912.
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                                                                                                                                2001JP-0277314
                                                                                                                                                                                                                                                                    Fukushima N, Tsuchiya M,
                                                                                                                                                                                                (CHUS ) CHUGAI SEIYAKU KK
                                                                                                                                                                                                                                                                                                                                    WPI; 2002-682599/73.
P-PSDB; ABG97832.
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hes 337; Conserv
                                                                                                                                12-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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Matches
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ABK71405
ID ABK71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCA---CTTTGTTA
                                                     The present sequence is that of patient-specific bicistronic chimeric idiotype VR.642 (plasmid VAXID), which is used to treat B-cell lymphoma patients. The plasmid includes the cytomegalovirus immediate-early promoter, enhancer and 5' untranslated sequences, driving the expression of mouse-human chimeric immunoglobulin light and heavy chain sequences. The human light and heavy chain sequences. The bound cell lymphom cell line RAMOS. The transcriptional terminator region includes polyA and termination signals from the bovine growth hormone gene. According to the invention, co-administration of VR1642 with a plasmid (see AAF30314) encoding human Fms-like Lyrosine kinase (R1t-3 ligand) provides a means of treating a patient with B-cell lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 7528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7528 BP; 1896 A; 1980 C; 1847 G; 1805 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 78.8%; Score 307.2; DB 2
Best Local Similarity 88.3%; Pred. No. 1.2e-83;
Matches 346; Conservative 0; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trcggaagagacccggrrgaccgrccragg 389
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241 AATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300

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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes a modified antibody comprising at least 2 heavy chain variable domains and 2 or more light chain variable domains of an antibody, and exhibits thrombopoietin (FPO) agonistic effect by causing the TPO receptor to crosslink. The antibodies are useful in preventives and/or remedies for platelet reduction-associated blood diseases, thrombocytopenia following cancer chemotherapy or leukaemia. The antibody can act as a FPO signal transduction agonist by transducing a signal into cells by crosslinking a TPO receptor to exert TPO agonism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                       thrombocytopenia, cancer chemotherapy; leukaemia; signal transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGGCAAAGCCCCCAAACTCATGATTTATGAGGCCAGTAAACGGCCCTCAGGGGTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Degraded thrombopoietin agonist antibodies containing H and L chain V domains of monoclonal antibody, useful in preventives and/or remedies for blood diseases, thrombocytopenia following cancer chemotherapy or
                                                            DNA encoding thrombopoietin agonist antibody associated protein #25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
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                                                                                          antibody, thrombopoietin, TPO; agonist, ptor; platelet reduction-associated blood disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                               Orita T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 387 BP; 79 A; 124 C; 95 G; 89 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                               Tsunoda H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                               Yabuta N,
                                                                                                                                                                                                                                                                                                20-OCT-2000; 2000JP-0321821.
17-APR-2001; 2001WO-JP03288.
12-SEP-2001; 2001JP-0277314.
                                                                                                                                                                                                                                                                  22-OCT-2001; 2001WO-JP09259.
                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                (CHUS ) CHUGAI SEIYAKU KK
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                                                                                                                                                                                                                                                                                                                                                                                               Fauchiya M, Obtomo T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 337; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                              2002-383513/41
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-383513/
P-PSDB; ABG35333.
                                                                                                                                                                                                    WO200233072-A1
                                                                                                          TPO receptor;
                             30-JUL-2002
                                                                                                                                                                                                                                   25-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leukaemia
ABK71405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                          Modified
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                                                                                                                                           gene; da
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The invention relates to isolated polynucleotide (1) and polypeptide (11) sequences. (1) is useful as hybridisation probes, polymerase chain reaction (PRR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (11). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (11) or to treat disease states involving (11). (11) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (11) and its binding partners are useful in medical imaging of sites expressing (11). (1 and (11) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity
                                                                          301 Gergadeadeadergarrarracrecadercararacaaccadaadeacrecadarre 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnostic coding sequences of the invention.
Note: The sequence data for this patent did not appear in the printed
specification, but was obtained in electronic format directly from WIPO
301 GCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome mapping; gene mapping; gene therapy; forensic; upplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding novel human diagnostic protein #19281.
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                                                                                                                                                                       387
                                                                                                                                                                                                                                                  361 GGCGGAGGACCAAGCTGACCGTCCTA 387
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                                                                                                                                                                       361 GGAAGAGGGACCCGGTTGACCGTCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS83477 standard; cDNA; 756
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
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13-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 AGTGGTTCTGGGTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300
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                                                                                                          ATGGCCTGGACTCTCGTCGTCACCTCCTCACGGCACAGGATCCTGGGCTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
                                                         ô
Length 756;
Score 306.8; DB 23; Length
Pred. No. 6.9e-84;
0; Mismatches 52; Indels
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  78.7%;
86.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0540217.
2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
Query Match
Best Local Similarity 86.7
Matches 338; Conservative
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P-PSDB; ABG22850.
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23-AUG-2000;
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polymerase contain reaction (FLK, primers), uniquency, configurately contain reaction of (II). The polymerase can also used in diagnostics as expressed sequence tags to relative expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and canno acid sequences. AASéA197-AAS94564 represent novel human call sequences date for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC 180
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primers, oligomers, and for chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGGCCTGGACTCTGCTCCTCGTCACTCACTCAGGGCACAGGATCCTGGGCTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.7%; Score 306.8; DB 2
86.7%; Pred. No. 7.2e-84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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Best Local Similarity 86.7
Matches 338; Conservative
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Search completed: December 29, 2003, 16:25:33 Job time : 172.16 secs

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TCTGCCCTGACTCAGCCTGCCTCCGTGTCTTGGTCTCTTGGACAGTCGATCACCATCTCC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGCCTGGGCTCTGCTGCTCTCACCCTCCTCAGGGCACAGGGTCCTGGGCCCAG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the predictation or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

(e) selecting a composition for inhibiting prostate cancer in a patient;

(f) assessing the prostate call carcinogenic potential of a compound;

(g) determining whether prostate cancer has metastasized in a patient;

(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGGCCTGGACTCTGCTCCTCGTCACCCTCCTCACGGGCACAGGATCCTGGGCTCAG 60
                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   patient;(I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.3%; Score 305.4; DB 23; Length
89.2%; Pred. No. 2.5e-83;
ive 0; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1636 BP; 345 A; 470 C; 479 G; 342 T; 0 other;
                                                                                                                                                                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 3949; 11750pp; English
                                                                                                                                                                                                                                     Schlegel R, Endege WO, Monahan JE;
                                                                        16-MAR-2000; 2000US-189862P-25-MAY-2000; 2000US-207454P-09-JUN-2000; 2000US-211314P-13-DEC-2000; 2000US-255281P-
                  20-FEB-2001; 2001WO-US05171
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Best Local Similarity 89.2
Matches 354; Conservative
                                                                                                                                                                                                                                                                            WPI; 2001-662795/76
                                                       17-FEB-2000;
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TGCACTGGAACCAGCGATGACGTTGGTGGTTATAA-CTATGTCTCCTGGTACCAACACA 179 239 cccaggcaaagcccccaaacrcargarrrargargrcagraarcgcccrcagggrrrc 299 TGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGGCTCCA 299 TAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCA 359 TGCACTGGAACCAGCAGTGACATTGGGGGTTATAACCTATGTCTCCTGGTATCAACAACA 239 comprising CCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTC 7; Gaps

GCCTGAGGACGAGGCTGATTATTACTGCAGCTCATATACAAGCAGCAGCAGCACTCTTT 419

GTTATTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 390 rererregaacregaaccaagereaccerecraegr 456

GGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACT----TT

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

						SUMMARIES	
	Result No.	Score	Query Match	Query Match Length	DB	QΙ	Description
	:	328.6	٦.	4	6	AF416358	358 Papio
	7	32	77.3	441	σ	AF416359	F416359 Papic
	m	323.8	76.5	420	6	MMU57560	Macaca
	41	319	75.4	420	σ,	MMU57565	
	ń			411	σ.	MMU57563	Macaca mul
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	- (			414		MMU5/568	
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	o .		•	1431	ه د	AK265201	ARZ65ZUI Sequence
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	7.6	512.4		977	ם ע	AFOSZIZO HETCHYYJE	
	13	310		420	ח ס		M99607 Human (clon
	4 -	3.908	73.2	468	. 0	HUMIGHZE	man
	15	305.6		414	σ	HST22X26	Z75399 H.sapiens m
	16	305		414	σ	HSIGHXX23	sapi
-	17	303.4	71.7	435	σ	MMU57566	caca
	18	302.8	71.6	423	σ	AF174036	AF174036 Homo sapi
	19	301.8		432	δ	HSIGHXX26	sapie
	20	301.2		423	σ	HSIGHXX20	
	21	299.8	70.9	1404	ø	AR135375	
	22	299.8		1404	9	AR135376	
	23	299.8		1404	9	AR135377	
	24	299.6		423	σ	AF062258	AF062258 Homo sapi
	25	299.6		486	σ	AF417843	Ното зар
	26	298.6		423	σ,	HST14X12	Ξį
	27	298.2	70.5	423	9	AR008995	95 Sequence
	28	298.2		423	φ·	161194	Sequence
	29	298.2		423	9	·	1/8/43 Sequence 19
	30	298.2		453	σ,	HSE5444	ᆣ.
	31	298.2		2149	σ,	BC011857	
	35	297.6	70.4	447	σ,	AF416357	
	33	297		423	σ	HST14X24	l.sapie
	34	296.6	70.1	429	σ	AF062232	
	32	296.6	70.1	481	9	BD182342	Anti
	36	296.4	70.1	619	9	AX427527	
	37	295.2		420	9	AR006813	m
	38	295.2		420	9	AR135372	
	39	295.2	69.8	420	9	171325	O)
	40		69.7	420	σ	AF062220	Ношо вар
	41	294.8		423	σ	HSIGHXX29	911 Н.
	42	g,	69.7	426	σ	AF062278	62278 Homo sap
	43	9	9.69	4	σ	HSIGHXX27	9 H.sapiens
	44	292.4	69.1		9	988	08863
	45	σ	69.1	1431	ø	AR265197	AR265197 Sequence
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## ALIGNMENTS

RESULT 1 AF416358 LOCUS DEFINITION ACCESSION	AF416358  Papio cynocephalus anubis clone VH4-4 immunoglobulin heavy chain variable region mRNA, partial cds.
VERSION KEYWORDS SOURCE ORGANISM	AF416358.1 GI:19744277 Papio anubis (olive baboon) Papio anubis
REFERENCE AUTHORS	<pre>Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Papio. 1 (bases 1 to 435) Scinicariello,F., Jayashankar,L. and Attanasio,R.</pre>

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GTCTCCTCA
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GGSISSSXWSWTRQAPGKGLBWIGGIYSNSGWYYYNPSLKNRVTISTDTSKNQFSLKL
SSVTAADTAVYYCARDLGAYNWGPQHYWGQGVLVTVSSASASA"

131 c 131 c 131 g 92 t
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                                                                                   2 (bases 1 to 435)
Scinicariello,F., Jayashankar,L. and Attanasio,R.
Direct Submission
Submitted (04-SEP-2001) Department of Biology, Ge
University, PO BOX 4010, Atlanta, GA 30302, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                    Score 328.6; DB 9;
Pred. No. 1.7e-78;
0; Mismatches 49;
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/product="immnoglobulin heavy
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/db_xref="G1:19744278"
                                                                                                                                                                        /organism="Papio anubis"

mol_type="mRNA"

shb_species="anubis"

/db_xref="taxon:9555"

/clone="VH4-4"
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variable region mRNA, partial cds.
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Best Local Similarity 87.7%;
Matches 371; Conservative
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/db_xref="G1:19744280"
/db_xref="G1:19744280"
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GGSISSGYYWSWIRQPPGKGLEWIGNIDGNSASTNYNPSLKNRVTISKDTSKNQFSLK
LSSVTAADDTAVYYSMATYSGNYKYGLDAWGGGVVYTVSSASAS"

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1 (bases 1 to 441)
Scinicariello,F., Jayashankar,L. and Attanasio,R. Baboni immunoglobulin variable region heavy chains: identification of genes homologous to members of the human IGHVI-IGHV7 subgrouppenetics 53 (10-11), 815-820 (2002)
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Pred. No. 4.7e-78;
0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 441)
Scinicariello,F., Jayashankar,L. and Attanasio,R.
Direct Submission
Submitted (04-SEP-2001) Department of Biology, Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University, PO BOX 4010, Atlanta, GA 30302, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .441
/organism="Papio anubis"
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/sub_species="anubis"
/db xref="taxon:9555"
/clone="VH4-7"
Papio anubis (olive baboon)
Papio anubis
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Best Local Similarity 86.9%;
Matches 373; Conservative
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417

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SSVTAADTAVYYCARGDYSSNWWYFEFWGQGALVTVSS"
123 c 128 g 89 t
                                                                                                                                                                                                                                                                                                                       PRI 11-FEB-1998
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                                                                                                                                                                                                                                                                                     ימיוט /ספל (ימינט 420 pp mRNA linear PRI 11-FBB-1998 Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC antibody, mRNA, partial cds.
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and Capra, J.D.
Direct Submission
Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center, University of Texas Southwestern Medical Center, 6000 Harry Hines Blvd., Dallas, TX 75235-9140, USA
Location/Qualifiers
361 GCCCAAAIAGCIGGAACAACGCIAGGCIICIGGGGCCAGGGAGICCIGGICACCGICICC 420
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Catarrhini; Cercopithecidae;
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1 (bases 1 to 420)

Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Roubinet Blancher, A. and Capra, J.D.
Variable region gene segment utilization in rhesus monkey hybridomas producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34)

97368199
                              1 ATGAAACACCTGTGGTTCTTCCTCCTCGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
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ilarity 86.3%; Pred. No. 7e-76;
Conservative 0; Mismatches 55; Indels
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/codon_start=1
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/proctein_id="AAC02642.1"
/db_xref="G1:1575078"
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/db_xref="taxon:9544"
/note="hybridoma 1C9"
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Macaca mulatta
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GYSISSGYGWNWIRQPPGKGLEWIGSIGGSRGNTNHNPSLKSRVTISIDTSKNQFSLK
LRSLTAADTAVFYCARDGGYSSRFFDYWGQGVLVTVSS"
                                                                                                                                                                                                                                                          Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
1 (bases 1 to 420)
Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Roubinet, F., Blancher, A. and Capra, J.D.
Variable region gene segment utilization in rhesus monkey hybridomas producing human red blood cell-specific antibodies:
Mol. Immunol. 34 (3), 237-253 (1997)
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                                    PRI 11-FEB-1998
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Macaca mulatta ig rearranged heavy chain variable region, anti-RBC
antibody, mRNA, partial cds.
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Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
and Capra, J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
University of Tess Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 75235-9140, USA
Location/Qualifiers
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Codon start=1

product="immunoglobulin heavy chain"

protein id="AACO2637.1"

db_xref="GI:1575068"
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Pred. No. 3.5e-77;
0; Mismatches 52
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/organism="Macaca mulatta"
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/db_xref="taxon:9544"
/note="hybridoma 1C8"
                                                                                                                                                                                                      Macaca mulatta (rhesus monkey)
Macaca mulatta
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                                                                                                                         U57560
U57560.1 GI:1575067
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93232287
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/cell type="pre-B"
/tissue type="bone marrow"
/clone_lib="LE library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="diversity region"
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/note="joining region"
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/db_xref="taxon:9606"
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/note="variable r
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diversity region; Ig he
variable region.
Homo sapiens (human)
Homo sapiens
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1 (bases 1 to 411)
Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Roubinet,F., Blancher,A. and Capra,J.D.
Variable region gene segment utilization in rhesus monkey hybridomas producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34)
Mol. Immunol. 34 (3), 237-253 (1997)
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/codon start=1
/product="immunoglobulin heavy chain"
/product="immunoglobulin heavy chain"
/product="immunoglobulin heavy chain"
/db_xref="c1:1575074"
/db_xref="c1:1575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             411 bp mRNA linear PRI 11-FEB-1998
Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC
antibody, mRNA, partial cds.
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                                                          AACCCGTCCTCAAGAGTCGAGTCATTTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
                                                                                           CTGAACCTGAACTCTGTGACCGCCGCGCGCACACGCCGTGTATTACTGTGCCAGAGATTGG 360
                                                                                                                                                                                                  GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 420
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Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
and Capra, J.D.
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Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
Submitted (106-MAY-1996) J.S. Andris, Molecular Immunology Center,
University of Texas Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 75235-9140, USA
Location/Qualifiers
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Pred. No. 1.2e-75;
0; Mismatches 38; Indels 12;
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/organism="Macaca mulatta"
/mol_type="mRNA"
/db_xref="taxon:9544"
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Best Local Similarity 88.2%;
Matches 373; Conservative
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FEATURES

RESULT 5 MMUS7563

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423 bp mRNA linear PRI 26-JUL-1997
H.sapiens mRNA for XLA IG heavy chain VDJ region (LE 4-8).
X65910 S58678
                                                                                                                                                                                                                                                                 178 CCAGGGAAAGGGACTGGAGTGGATTGGACGTTTCTATGGTACTAGTGGGAGCACCTACTAT 237
                                                                                                                                                                                                                                                                                                                                                     241 AACCCGTCCCTCAAGAGTCGAGTCATTTCACAAGACAGGTCCAAGAACCAGTTCTCC 300
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61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
                                                                                             TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC 180
                                                                                                                               CCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACTAC 240
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 423)
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Submitted (08-APR-1992) C. Schiff, Centre D'Immunologie de Marseille, Case 906, 13288 Marseille, Cedes 9, FRANCE
2 (bases 1 to 423)
Milili,M., Le Deist,F., de Saint-Basile,G., Fischer,A., Fougereau,M. and Schiff,C.
Bone marrow cells in X-linked agammaglobulinemia express pre-B-specific genes (lambda-like and V pre-B) and present immunoglobulin V-D-J gene usage strongly biased to a fetal-like
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420

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COUNT

BASE CC ORIGIN

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1. .414
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/translation="MRHWFFLILVVAPRWVLSQVQLQESGPCLVKPSETLSITCAVS
SSYTAADTAVYYSWIRQPPGRGLEWIGYIYGSGSAYYNPSIKSRVTISIDTSKNQFSLKL
SSYTAADTAVYYSCHOPYGPPYFPWGGVLVTVSS"
a 128 c 110 g 93 t
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                                                                                                                                                                                                                                                                                                               1 ATGAAACACCTGTGGTTCTTCCTCCTCCTCGTGGTAGCTCCCCAGATGGGTCCTGTCGTCCCAG
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Pred. No. 2.6e-74;
                                                                                                                                                                                                                      Score 314.6; DB 9
Pred. No. 1.1e-74;
0; Mismatches 44
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from patent US 6113898.
xref="taxon:9544"
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462 c 385 g
                /note="hybridoma"
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84.5%;
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Best Local Similarity 87.5%;
Matches 370; Conservative
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AR108867
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1 (Dases I to 414)
Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Roubinet, F.,
Blancher, A. and Capra, J.D.
Variable region gene segment utilization in rhesus monkey
hybridomas producing human red blood cell-specific antibodies:
Mol. Immunol. 34 (3), 237-253 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MMU57568 414 bp mRNA linear PRI 11-FEB-1998
Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC
antibody, mRNA, partial cds.
                                                                                      2,
                                                                                                                                                                                                                 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGACACCCTGTCCCTCACC 120
                                                                                                                                                                                                                                                                                  CTGAACCTGAACTCTGTGACCGCCGCGGGACACGCCCGTGTATTACTGTGCCAGAGATTGG 360
                                                                                                                                                                                         CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
                                                                                                                                                                                                                                                              TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC 180
                                                                                                                                                                                                                                                                                                                                   CCAGGGAAGGGACTGGAGTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACTAC 240
                                                                                                                                                                                                                                                                                                                                                     CCAGGGGAAGGGCTGGAGTGGATTGGGGAAATCTATCATA---GTGGGAGCACCAACTAC 237
                                                                                                                                                                                                                                                                                                                                                                                                    AACCCGTCCCTCAAGAGTCGAGTCATTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
                                                                                                                                                                                                                                                                                                                                                                                                                         GCCCAAATAGCTGG---AACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTC 417
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Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Blancher,A.
and Capra,J.D.
Direct Submission
                                                                                                                                         1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCTCAG 60
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Macaca mulatta
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center, University of Faxas Southwestern Medical Center, 6000 Harry Hines Blvd., Dallas, TX 75:55-5140, USA Location/Qualifiers
                                                                                                                       1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
                                                                                        Gaps
                                                                                      9
                                                      423;
                                                      Length
                                                                                      Indels
                                                  ore 315.6; DB 9;
ed. No. 5.9e-75;
Mismatches 49;
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/organism="Macaca mulatta"
/mol_type="mRNA"
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nilarity 87.1%;
Conservative 0
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     84
                                                  Query Match
Best Local Simi
Matches 371;
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418

418

LOCUS DEFINITION

RESULT 7 MMU57568 VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS

TITLE

Bource

FEATURES

JOURNAL MEDLINE PUBMED

REFERENCE AUTHORS

TITLE JOURNAL

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Howaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 1431)

S Anderson, D.R., Hanna, N., Brams, P. and Hard, C. Identification of unique binding interactions between certain antibodies and the human B7.1 and B7.2 co-stimulatory antigens antibodies and the human B7.1 and B7.2 co-stimulatory antigens antibodies and the human B7.1 and B7.2 co-stimulatory antigens by D 2001504693-A/6

PN 70 2001504693-A/6

PN 10-APR-2001

PF 29-OCT-1997 UP 1998521633

PR 08-NOV-1996 US 08/746361

PI DARRELL RAUBERSON, NABIL HANNA, PETER BRAMS, CHERYL HARD PC A61X39/395, CO7X16/18, CO7X16/28

CC Strandedness: Single;

CC Strandedness: Single;

CC Topology: Linear;

FH Key

FT CDS
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                                                                        CTGAACCTGAACTCTGTGACCGCCGCGGACACGCCGTGTATTACTGTGCCAGAGATTGG 360
                                                                                                                                                                 CTGAAGCTGAACTCTATGACCGCGCGGACACGGCCGTGTTTACTGTGTGAGAGATGT 360
                                           AACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACCACGTCCAAGAACCAGTTCTCC 300
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181 CCAGGGAAGGGGCTGGAGTGGGAGTTTCTATAGTAGTAGTGGGAACACCTACTAC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BD063039 1631 bp DNA linear PAT 27-AUG-Identification of unique binding interactions between certain antibodies and the human B7.1 and B7.2 co-stimulatory antigens.
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74.0%; Score 313.2; DB 6; Length 1431;
Best Local Similarity 84.5%; Pred. No. 2.6e-74;
Matches 370; Conservative 0; Mismatches 53; Indels 15;
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Organism="Homo sapiens"
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db xref="texon:9606"
a 463 c 384 g 265
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Location/Qualifiers
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JP 2001504693-A/6.
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Homo sapiens
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                                                ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
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Method for producing polyhydroxyalkanoates in producing polyhydroxyalkanoates in producing polyh
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84.5%; Pred. No. 2.6e-74;
ive 0; Mismatches 53
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AR265201
AR265201.1 GI:29693622
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Best Local Similarity 84.5
Matches 370; Conservative
  370; Conservative
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/clone="LE 4-5"
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 Mismatches
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/db_xref="taxon:9606"
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diversity region; Ig h
variable region.
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Home sapiens
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/protein_id="AAC18156.1"
/db_xref="cd:3170703"
/translation="MXHIMFPLLLVAAPRWVLSQVQLQESGPGLVKPSGTLSLTCAVS
GGSISSNWWGNVPQPGKGLEWIGEIYHSGSTNYNPBLKSRVTISVDKSKNOFSLKL
SSVTAADTAVYYCARGPPDYGDYRYFDYWGQGTLVTVSSG"
                                                                                                                                                                                                                                                                                   AFU62120
Homo sapiens clone 21u-39 immunoglobulin heavy chain variable region (IGH) mRNA, partial cds.
                           CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGATTGG 360
                                                                                                  CTGAAGCTGAACTCTATGACCGCGGGGGCCGTGTATTACTGTGTGAGAGATCGT 360
                                                                                                                                         405
                                                                                                                                                                  CTTTTTTCAGTTGTTGGATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGGAGTC 420
 181 CCAGGGAAGGGCCTGGAGTGGATTGGAGTTTCTATAGTAGTAGTGGGAACACCTACTAC 240
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1 (bases 1 to 426)
1 (bases 1 to 426)
1 (mang,X. and Stollar,B.D.
1 Immunoglobulin VH gene expression in human aging Clin. Immunol. 93 (2), 132-142 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang.X. and Stollar, B.D. Direct Submission Submission Submission Submission Submission Submission Far. 1998) Biochemistry Department, Tufts University School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
                                                                                                                                         ------CGCTAGGCTTCTGGGGCCAGGGAGTC
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tissue_type="blood"
note="from elderly repertoire 21u"
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1. .426
/organism="Homo sapiens"
/dol_type="mRNA"
/db zref="taxon:9606"
/chromosome="14"
/map="14q32.33"
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/gene="IGH"
58. .>47£
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86.6%;
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PRI 26-JUL-1997
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 420)
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Submission
Submitted (08-APR-1992) C. Schiff, Centre D'Immunologie de
Submitted (08-APR-1992) C. Schiff, Centre D'Immunologie de
Marseille, Case 906, 13288 Marseille, Cedes 9, FRANCE
2 (bases 1 to 420)
Milli,M., Le Deist,F., de Saint-Basile,G., Fischer,A.,
Milli,M., Le Deist,F., de Saint-Basile,G., Fischer,A.,
Fougereau,M. and Schiff,C.
Bone marrow cells in X-linked agammaglobulinemia express
pre-B-specific genes (lambda-like and V pre-B) and present
immunoglobulin V-D-J gene usage strongly biased to a fetal-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCAGCTGCAGGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC
1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
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H.sapiens mRNA for XLA IG heavy chain VDJ region (LE 4-5)
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| Capen="10quva" |

| Codon_start=1 |

| product="immunoglobulin heavy chain" |

| protein id="AAA5298.1" |

| db_xref="G1:185496" |

| db_xref="G1:185496" |

| db_xref="G1:185496" |

| db_xref="G1:185496" |

| db_xref="G1:18596" |

| dc_xref="G1:18596" |

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/cell_type="B lymphocytes"
/tissue_type="blood"
/dev_stage="adult"
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/note="G00-128-528"
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/note="G00-128-528"
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/gene="IGHV@"
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Best Local Similarity
Matches 359; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGAACCTGAACTCTGTGACCGCCGCGGGACACGGCCGTGTATTACTGTGCCAGAGATTGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V-region; complementarity determining region; immunoglobulin heavy chain; processed gene. Homo sapiens (human) Homo sapiens (human)
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Human (clone R5A3H) Ig rearranged H-chain mRNA V-region, 5' end
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                                                                                                                                                                                                                                                                   Length 420;
                                                                                                                                                                                                                                                             73.5%; Score 311; DB 9; Length 42
85.1%; Pred. No. 1e-73;
ive 0; Mismatches 60; Indels
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/mol_type="mRNA"
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/map="14q32.33"
/sex="female"
           58. .352
/note="variable region"
353. .364
/note="diversity region"
                                                                                                                    365. .420
/note="joining region"
123 c 127 g
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Best Local Similarity 85.1
Matches 360; Conservative
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ACCESSION
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KEYWORDS
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TITLE
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HUMIGHRH
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SOURCE

LOCUS

120

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NY 275399

NY 275399.

ST5399.1 GI:2062062

immunoglobulin; immunoglobulin heavy chain; immunoglobulin

superfamily; variable region.

Homo sapiens (human)

Homo sapiens (human)

Homo sapiens (human)

Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Is (bases 1 to 414)

STONNELLS,C., D'Ercole,C., Depraetere,V., Metras,D., Boubli,L. and Pougereau,M.

Human thymic B cells largely overexpress the VH4 Ig gene family. A possible role in the control of tolerance in situ?
                                                                                                                                                                                                  ST22X26 414 bp mRNA linear PRI 30-APR-1997 sapiens mRNA for Ig heavy chain variable region (VH4DJ) (clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCTCACC 120
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361 GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCCAGGGAGTCCTGGTCACCGTCTCC 420
                   1 Argadacaccrerererrerrerrerrerresresrescreecastres and argadacreecastres
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (26-UUN-1996) Cecile Tonnelle, Centre d'Immunologie
Marseille Luminy, Marseille, 13288, France
Location/Qualifiers
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1. .414
/product="Ig heavy chain variable region (VH4DJ)"
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Pred. No. 3.1e-72;
0; Mismatches 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. 414
/organism="Homo sapiens"
/organism="Homo sapiens"
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/chromosome="14"
/clone="T22.26"
/tissue type="b-lymphocyte"
/tissue type="thymus"
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Best Local Similarity 86.3%;
Matches 364; Conservative
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Tonnelle, C.
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57. .351
/note="Ig '
352. .375
376. .414
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SSVTAADTAVYYCARGHSSSWARDYWQGTLVTVSSGSASAP"
118 c 139 g t
                 אפר-JUL-1994 mRNA linear PRI 27-JUL-1994 Human immunoglobulin heavy chain variable region (VH IV family) אוניסה וקאור from IgM rheumatoid factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGGGACCCTGTCCCTCACC 157
                                                                                                          L29122.1 GI:465144 Tip heumatoid factor; variable region subgroup VH-IV sapiens (human) Homo sapiens (human) Homo sapiens
                                                                                                                                                                                 Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 468)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCTCAG 97
                                                                                                                                                                                                                                                                     Human rheumatoid factors with restrictive specificity for rabbit immunoglobulin G: auto- and multi-reactivity, diverse VH gene segment usage and preferential usage of V lambda IIIb J. Exp. Med. 179 (5), 1445-1456 (1994)
                                                                                                                                                                                                                                    Fang, O., Kannapell, C.C., Gaskin, F., Solomon, A., Koopman, W.J. and Fu, S.M.
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ilarity 86.8%;
Conservative (
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Qy 241 AACCCGTCCTCAAGAGTCGATTGATTACACA---GTGGGAGCACCAACTTCC 300

238 AACCCGTCCTCAAGAGTCGAGTCACCATACACAGAACCAGTTCTCC 297

Qy 301 CTGAACCTGAACTCTGACCGCGCGCACACTATACAGAACCAGAACCAGTTTCC 297

Qy 302 CTGAAGCTGACCTGTGACCGCGCGCACACGTATTACTGTGCCAAGAATTGC 357

Qy 361 GCCCAAATAGCTGGACACGCGCGGACACGCGTGTATTACTGTGCGAAGATTAC 357

Qy 361 GCCCAAATAGCTGGAACAACGCTAGGGCCAGGGAGTCCTGGTCCCGTCTCC 420

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Qy 421 TC 422

Db 412 TC 413

Search completed: December 29, 2003, 19:01:24

Job time: 1755.27 secs
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Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB e Maximum DB e

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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 453)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapb-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

CLONe distribution: M.G. Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: Ml3 Forward.
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UI-HF-BKO-aal-c-02-0-UI.rl NIH MGC_36 Homo sapiens cDNA clone
IMAGE:3053955 5', mRNA sequence.
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TITLE
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BX283435 BX283435
BG397580 602438620
BG685428 602637281
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                            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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em estov: *
em estop: *
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em estp: *
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Database

Query Match 1

Score

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301.6 301.4 301.4 299

BOT 2410 AGENCOURT BOT 10876 AGENCOURT BOT 1080 AGENCOURT CB13593 K - EST 018 CB13594 K - EST 018 CB13594 K - EST 018 BOT 1080 AGENCOURT BX3965052 BX365052 BX365052 BX365052 BX3965052 BX365093 BX396123 BX365052 BX3965052 BX365093 BY3965052 BX365093 BY3965052 BX365093 BY396502 BX365093 BY39612 BX39940 BOT 1080 AGENCOURT BOT 1080 AGENCOURT BOT 11653 AGENCOURT BOT 1181 AGENCOURT

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/organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE958G051281; IMAGE:4565020"
/clone="IMAG958G051281; IMAGE:4565020"
/lab host="Primary B-cells from tonsils (cell line)"
/lab host="DH10B (phage-resistant)"
/clone lib="WINH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5: adaptor: aGCACGAGG(0: Size-selected >500bp for average insert size 1:8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH MGC Library."
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/ShowLib.lp.lcgi/response?libNo-972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (cloneGrzpd.de) for further information. Seq primer:
pCMV-M13u, Primer Sequence: CGTTGTAAAACGACGCCAGT.
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Pred. No. 2.8e-66;
); Mismatches 56; Indels
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BX283435 NIH MGC 48 Homo sapiens cDNA clone IMAGP958G051281 ;
IMAGE:4565020, mRNA sequence.
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1 (bases 1 to 502)

Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.

Human UnigeneSet - RZPD3
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Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp958G051281.
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                                                                                                                                                                                                                                                                                                                                                                           Length 453;
                                                                                                                                                                                                                                                                                                                                                                                                              49; Indels
                                                                                                                                                                                                                                                                                                                                                                           Score 301.6; DB 9;
Pred. No. 2.4e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      423
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                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                        organism="Homo sapiens"
                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3053955"
                   cocation/Qualifiers
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86.9%;
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Homo sapiens
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JOURNAL
COMMENT
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BX283435
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KEYWORDS
SOURCE
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                   FEATURES
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/ Organism=-now Septems
/ mol type="mRNA"
/ db_xref="taxon:9606"
/ clone="INAGE:4764956"
/ tissue_type="primary B-cells from tonsils (cell line)"
/ lab host="DH10B (plage-resistant)"
/ clone=lib="NIH_MGC_48"
/ clone=lib="NIH_MGC_48"
/ lone="organ: B-cells, Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                BG685428 101-MGC_48 Homo sapiens cDNA clone IMAGE:4764956 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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                                             377 GGAGACATCTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACGTCTCC 436
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can b
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
a column: 21
High quality sequence stop: 637.
High quality sequence stop: 637.
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/lab host="primary B-cells from tonsils (cell line)"
/lab host="primary B-cells from tonsils (cell line)"
/clone_lib="NIH_MGC_48"
/note="organ: B-cells; vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXXhoI sites using the following 5' adaptor: GGGAGG(G). Size-selected -550bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscribt II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 862)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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  602438620F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565020 5'
                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 827.
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llarity 85.3%; Pred. No. 3.4e-66;
Conservative 0; Mismatches 56
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/db_xref="taxon:9606"
/clone="IMAGE:4565020"
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/clone="IMAGE:57660"
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/clone="IMAGE:57660"
/clone="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
/note="Organ: pooled lung and spleen; Library is oligo-dr
spleen, and 20-22 week male spleens. Library is oligo-dr
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb, Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."
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CTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 180
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NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
                                                                                                                                                                                                                                                                                                        298 TACAACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTC
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Tissue produrement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI2810 row. h column: 21
High quality sequence stop: 626.
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AGENCOURT 6839001 NIH MGC_122 Homo 15', mRNA Sequence.
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/db_xref="taxon:9606"
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/mol_type="mRNA"
/mol_type="mRNA"
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/dlone="CSODIO86YJ13"
/tissue_type="PLACENYA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENYA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENYA COT 25-NORMALIZED"
/note="lis strand cDNA was primed with a notI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
36 a 291 c 236 g 177 t
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COT 25-NORMALIZED Homo sapiens cDNA
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1 (bases 1 to 890)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOA1086CE07QPl&cluster=7198.r. Contact :
Feng Liang Email : fliangelifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOA1086CE07QPl.
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0; Mismatches 46; Indels
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/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lone lib="UTH MGC 113"
/note="Grgan: Spleen; Vector: pOTB7; Site 1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned
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MH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2516 row: n column: 16
High quality sequence stop: 560.
                                                                                                            5 AACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAGCTGC
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smatches 56;
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Tissue Procurement: Dr. Mark Watson
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 197
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II (Life Technologies). Note: this is a
NIH MGC Library."
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Catarrhini; Hominidae; Homo.
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Tissue Procurement: Dr. Mark Watson
cDNA library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM518 row: n column: 14
High quality sequence start: 10
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia, Eutheria, Primates,
1 (bases 1 to 921)
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Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                           This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s wiemann@dkfz-heidelberg.de; sequenced by MediGenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 532;
                                                                                                                                                                   Mewes H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al agguence also available.
This clone (DKFZp686M10219) is available at the RZPD in Ber
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
14059 Berlin-Charlottenburg, GBRMANY; Email: clone@rzpd.de
                                                                                                                                                                                                                                                             Submitted (07-MAY-2003) to the EMBL/GenBank/DDBJ databases MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
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Pred. No. 2.4e-64;
0; Mismatches 63;
                                                                                                                                                                Ottenwaelder B., Obermaier B., Deutschenbaur S.,
Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="cDNA-collection"
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Best Local Similarity 83.8%;
Matches 357; Conservative 0
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                                                                                                                                                                                                    /clone="IMAGE:6302029"
/lab_host="DH10B (phage-resistant)"
/clone lib="NNH MGC 113"
/note="Organ apleen; Vector: pOTB7; Site 1: XhoI; Site 2:
BCORI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M within (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
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Pred. No. 2.7e-64;
0; Mismatches 60;
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Last updated, Version 1)
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                                                                                                       organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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adjusted to have about bure Line CDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2.000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5, primer and N(dT)14 as 3, primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded CDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted CDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Toplof, with
                                                                                                                                                                                 467 bp mRNA linear EST 29-JAN-2003
K-EST0191378 L7N800102s1 Homo sapiens cDNA clone L7N800102s1-6-D11
5', mRNA sequence.
CB138507
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//clone_lib=_L788010281"
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Site_2: NotI; The poly (A+* RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The CDNA vector was
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1 (bases 1 to 467)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-44409
Email: yongeung@mail.kribb.re.kr
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High quality sequence stop: 467.
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Homo sapiens
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                             TCA 423
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                             1201 bp mRNA linear EST 08-MAY-2003
ACENTA COT 25-NORMALIZED Homo sapiens CDNA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
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/clone_lib="Homo sapiens Placenta cor 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dr)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
356 c 298 g 226 t 56 others
                                                                                                                                                                                                                                                                                                                                                                                                                                         Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: sequefegenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198 r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI001CE07QPlccluster=7198 r. Contact :
freps.frwing Email: fliangelifetech.com URL :
http://fulllength.invitrogen.com/ luvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI001CE07QPl.
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Pred. No. 6.6e-64;
0; Mismatches 44; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                   Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
                                                    BX377045 Homo sapiens PLACENTA COT 25-NORV clone CS0D1001YJ13 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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Best Local Similarity 86.1%;
Matches 364; Conservative (
                                                                                                                                                                                                sapiens (human)
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/clone lib="L7N80010281"
/note="Organ: Liver; Vector: pCNS-D2; Site 1: ECORI; Site 2"Not!; The pOly (A)* RAW was dephosphorylated with bacterial alkaline poly (A)* RAW was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECORI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The CDNA vector was adjusted to have about 6ndr. The CDNA vector was acicularized with E. coli DNA ligase after digestion of ECORI which site is also included in vector. An RNA strand converted to a DNA strand by Okeyama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method. The CDNA libraries constructed by this method are full-length enriched CDNA libraries of the method of S,000 colonies in original CDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of blotinylated angle stranded CDNA by in vitro transcription reaction. The synthesized RNA probes were constructed by transformation of the remaining DNA into competent cells E. coli ToplOF' with constructed by transformaion of the remaining DNA into competent cells E. coli ToplOF' with
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Pred. No. 7.9e-64;
0; Mismatches 62;
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Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
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K-EST0203106 L7N800102s1 Homo sapiens CDNA clone L7N800102s1-18-C09
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Korea Research Institute of Bioscience & Biotechnology
52 Escun-dong Vuseong-gu, Daejeon 305-333, South Korea
Tal: +82-42-860-4409
Fax: +82-42-860-4409
                                                                                                                                62; Indels
                                                      Score 291.8; DB 7
Pred. No. 7.5e-64
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Plate: 18 row: C column: 09
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Location/Qualifiers
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CB147325
                                                      Query Match
Best Local Similarity 83.99
Matches 355; Conservative
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//BD host="TOD10F""
//Clon lib="L5HLK1"
//Clon lib="L5HLK1"
//Clon lib="L5HLK1"
//Clon lib="L5HLK1"
//note="Organ: Liver; Vector: pCNS-D2; Site l: EcoRI;
Site_2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (RAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The GDNA vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coll DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The
                                                                                                                                                                                                                     Homo sapiens
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 537)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method. The CDNA libraries constructed by this method are full-length enriched cDNA library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
Sorea Research Unstitute of Daejeon 305-333, South Korea
Tel: +82-42-860-4470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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'db_xref="taxon:9606"
'clone="L5HLK1-27-F01"
                                                                                                              CB135937.1 GI:28103031
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                                                                                                                                                                                         Homo sapiens (human)
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Circularized with E. coli DNA ligase affer digestion of Ecots which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The converted to a DNA strand by Okayama-Berg method. The competent cells E. coli ToplOF' by electroporation of the CDNA libraries constructed by this method are sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by library, the abundant cDNAs were selected and amplified by promotor as 5' primer and N(dI)14 as 3' primer. The PCR
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/note="Organ: Liver; Vector: pCNS-D2; Site 1: EcoRI;
site 2: NotI; The poly (A+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA linker including strand cDNA was synthesized from oilgo dT-selected mRNA by priming with dT-tailed vector. The GL-tailed vector was adjusted to have about 60nt. The CDNA vector was
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K-EST0187880 L7N800102s1 Homo sapiens CDNA clone L7N800102s1-9-F04
5', mRNA sequence.
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241 AACCCGTCCACAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
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Genome Research Center
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52 Ecoun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Fax: +82-42-860-1409
Fax: +92-42-860-1409
Flate: 9 row: F column: 04
High quality sequence stop: 552.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="L7N80010281-9-F04"
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/organism="Homo sapiens"
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/lab host="Top10F'"
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products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli ToplOF' with electroporation method."
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57, mRNA sequence.
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Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Fax: +82-42-860-4470
                                                                                                                                                                                                                                                                                                                                                                                       Score 291.8; DB 14; DE 14: DE 15: DE 
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Best Local Similarity 83.9%;
Matches 355; Conservative
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/lab host="Top10F" |
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//lone=lib="L7880010281" |
//lone="Togan: Liver; Vector: pCNS-D2; Site_1: EcoRI;
//site_2: Not!; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was lagated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The CDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The converted to a DNA strand by Okayama-Berg method. The converted conflate constructed by this method are full-length enriched CDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNA swere selected and amplified by PCR reaction using vector region primer including T7 products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antiennes single stranded CDNAs probes were hybridised by electroporation method:

Ilbrary and incubated with avidin-gel. After removing DNA-libraries were constructed by transformation of the remaining DNA into competent cells E coli Toplof, with electroporation method.
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                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L7N80010281-21-A09"
Email: yongsung@mail.kribb.re.kr
Plate: 21 row: A column: 09
High quality sequence stop: 574.
Location/Qualifiers
                                                                                                                                                                             /organism="Homo
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Post-processing:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    monoclonal antibody binding human B7.1 or B7.2 antigen for treating autoimmune disease or graft-versus-host disease
                                                                                                                                                                                                             Primatised anti-human B7.1 antigen antibody 16C10 heavy chain DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.0%; Score 313.2; DB 18; Length 1431; 84.5%; Pred. No. 2.7e-71; ive 0; Mismatches 53; Indels 15;
                                                                                                                                                                                                                                                                   Monoclonal antibody; cynomolgus monkey; macaque; 16C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic luque erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma; ss.
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AAT62513 standard; DNA; 1431
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Chimeric Homo sapiens.
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                                                              300
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TGCGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGGCTGGATCCGCCAGCCC 180
                                                                                   AACCCTCCTCAAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTCTCC 300
                                                                                                                                                                                                                                                                                                                                                             Monoclonal antibody, Mab, macaque, heavy chain; primate, antigen, CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G; T cell proliferation; ss.
                                                              AACCCGTCCCTCAAGAGTCGAGTCATTTCACAAGACACGTCCAAGAACCAGTTCTCC
                                                                                                                                                    GCCCAAATAGCTGGAACAA-------CGCTAGGCTTCTGGGGCCAGGGAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B cells, e.g. graft rejection or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= 16C10 heavy chain
                                                                                                                                                                                                                                                                                                                                          Macaque primatized 16C10 heavy chain DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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T cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type idiabathic thrombocytopaenia purpura, systemic lupus erythematosus, type inflammatory bowel disease, allergy and multiple sclerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the MAA can be conjugated to a drug or toxin. MAA's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAA's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunosuppresses.
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Matches 370; Conservative
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- Macaca sp.
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CTGAACCTGAACTCTGTGACCGCCGCGGACACGCCGTGTATTACTGTGCCAGAGATTGG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGCAGTTGCAGGAGTCGGGCCCAGGAGTGGTGAAAGCCTTTGGAAGCCTGTCCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunogenicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
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                                                301 CTGAAGCTGAACTCTATGACCGCCGCGGACACGCCGTGTATTACTGTGTGAGAGATCGT
                                                                                                                                                                    --- CGCTAGGCTTCTGGGGCCAGGGAGTC
                                                                                                                                                                                                                                                CTTTTTTCAGTTGTTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCCGGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibodies containing donor complementarity determining regions and non-human primate acceptor frameworks, having reduced immunogenicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 85.0%; Pred. No. 2.6e-68; Similarity 85.0%; Pred. No. 2.6e-68; St. Conservative 0; Mismatches 58; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complementarity determining region; antibody; primate; immunoc
Old World ape; Old World monkey; antigen-binding affinity; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of Cynomologous VH cDNA clone 2-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 423 BP; 76 A; 125 C; 122 G; 100 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 79; 123pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP.
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                                                                                                                                                                        361 GCCCAAATAGCTGGAACAA-
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                                                                                                                                                                                                                                                                                                                                             CTGGTCACCGTCTCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ39331 standard; DNA; 423
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    301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CDB0) and/or B7.2 antigen (CDB6) for inducting the apoptosis of B7.4 cells. The invention is useful for treating diseases such as B cell cancer, lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell lymphoma, B cell lymphoma, a sell lymphoma, B cell sevencia purpura, systemic lupus, erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, allergy, multiple sclerosis or graft-vs-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or rejection of transplanted organ or tissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive airways disease, intestinal inflammations and allergies e.g. crohn's disease and ulcerative colitis, food related allergies e.g. migraine, rhinitis and eczema, and other types of allergies. The present nucleic acid sequence encodes the heavy chain of 16610, a primatised antibody used in the invention to induce apoptosis and inhibit production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
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Pred. No. 2.7e-71;
0; Mismatches 53; Indels
                                                                                             /*tag= a
/product= "Heavy chain of 16C10 antibody"
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        location/Qualifiers
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Matches 370; Conservative (
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show high affinity to human CD4, have little or no immunogenicity in humans and show reduced or absence of effector function. They can be used to treat autoimmune diseases such as rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.9%; Score 299.8; DB 18; Length 1404; 83.5%; Pred. No. 7.7e-68; ive 0; Mismatches 67; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 1404 BP; 312 A; 448 C; 377 G; 267 T; 0 other;
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                                                 Chimeric antibody comprising monkey variable domains and human constant domains - affects CD4-mediated immune functions, esp. useful for treatment of autoimmune disease, e.g. rheumatoid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 299.8; DB 1
Pred. No. 7.7e-68;
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                                                                                                                                         Disclosure; Page 86-88; 155pp; English
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Best Local Similarity 83.5%;
Matches 353; Conservative (
WPI; 1997-201913/18
                P-PSDB; AAW14926.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCCCCCAGATGGGTCTTGTCCCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequences (AAT62868-70) respectively code for the heavy chain regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S229P mutations. They can be used to provide novel monoclonal and chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in which the human IgG4 Fc binding domain framework is combined with the antigen binding domains (see also AAW1432-2.3) of macaque anti-human CD4 monoclonal antibody E9.1. These antibodies show high affinity to human CD4, have little or no immunogenicity in humans and show reduced or absence of effector function. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGCAGCTGCAGGAGTCGGGCCCCAGGAGTGAAGCCTTCGGAGACCCTGTCCCTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 AATCCCTCCACAACAATCGAGTCTCCATTTCAATAGACACGTCCAAGAACCTCTTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gamma-4E and -4PE mutations confer activity enhanced stability and eliminate depleting activity. The antibodies can be used to treat autoimmune diseases such as rheumatoid arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 18; Length 1404;
                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric antibody comprising monkey variable domains and human constant domains - affects CD4-mediated immune functions, espuseful for treatment of autoimmune disease, e.g. rheumatoid
CD4; monoclonal antibody; chimaeric antibody; recombinant anternologus monkey; autoimmune disease; rheumatoid arthritis; leukaemia; lymphoma; graft-versus-host disease; asthma; transplant rejection; HIV; therapy; CE9 gamma-4PE; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1404 BP; 313 A; 447 C; 379 G; 265 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 299.8; DB 18;
Pred. No. 7.7e-68;
0; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 91-93; 155pp; English.
                                                                                                                                                                                                                                                                                                               Reff ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.9%;
                                                                                                                                                                                                                                          95US-0523894.
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Matches 353; Conservative
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                                                                                                                                                                                                                                                                                                               Newman RA,
                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-201913/18
                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW14927
                                                                                                                                 WO9709351-A1
                                                                                                                                                                                                                                          06-SEP-1995;
                                                                                                                                                                   13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                          arthritis
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CCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACTAC
                                                                                                     ccedegaagesecresaaresarresaasrrrcraracracracresaaaracerrere
                                                                              241 AACCCGTCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC
                                                                                                                                                                                                                                             361 GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGGCCAGGGAGTCCTGGTCACCGTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR; amplify; clone; heavy; light; chain; variable; region; lambda; immortalised B-cell; vector; TCAE 6; human; IgGl; constant; antigen; recombinant; antibody; chimpanzee; Ig; Ag; old world monkey; eczema; immunoglobulin; therapeutic; rheumatoid arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant antibodies including Old World monkey portion and human portion - used for treatment of auto-immune diseases, infectious diseases, ALDS, tumours, diabetes, proliferative diseases, intestinal inflammations and allergies, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 53-54; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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92US-0856281.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
08-JUN-1993
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                     358 ATATTGAAATATCTTCACTGGTTATTATACTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 417
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GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides an antibody (Ab) comprising donor CDRs (complementarity determining regions) derived from a non-human antigenspecific donor antibody, and an acceptor framework from a non-human primate. The Abs are prepared by grafting CDRs from a non-human antigenspecific donor antibody onto homologous Old World ape or monkey acceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              frameworks. The Abs have reduced immunogenicity and are better tolerated in humans (because of the close similarity between the human and primate proteins), but retain the full antigen-binding affinity of the donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibodies containing donor complementarity determining regions and
non-human primate acceptor frameworks, having reduced immunogenicity in
                                                                                                                                                                                                                                                                                                                                                                                        Complementarity determining region; antibody; primate; immunogenicity; Old World ape; Old World monkey; antigen-binding affinity; 88.
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                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of Cynomologous VH cDNA clone 2-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 420 BP; 80 A; 125 C; 113 G; 102 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 84-85; 123pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                          AAZ39335 standard; DNA; 420 BP.
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                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                TCA 423
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                                                                                                                                                                                                                                                                                                          15-FEB-2000
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23-MAR-1992;
25-JAN-1995;
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                                                  Hanna N,
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                                                                                                                                                                                TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC 180
                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                   AACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
                                                                                                                                                                                                                                                                                                            CTGAACCTGAACTCTGTGACCGCCGCGGACACGCCGTGTATTACTGTGCCAGAGATTGG 360
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                                                                                                                                       CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
                                                                                                                                                    124 TGCAGTGTCTCTGGTGGCTCCATCAGCGGTGACTATTATTGGTTCTGGATCCGCCAGTCC 183
                                                                                                                                                                                                                                             CCAGGGAAGGGACTGGAGTGGATCGGCTACATCTATGGCAGTGGTGGGGGCACCCAATTAC 243
                                                                                                                                                                                                                                                                                       AATCCCTCCTCAACAATCGAGTCTCCATTTCAATAGACACGTCCAAGAACCTCTTCTCC 303
                                                                                             1 ATGAAACACCTGTGGTTCTTCCTCCTGCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
                                                                                                                 63
                                                                                                                   4 Argamacaccreregricurecrecrecreserescasececeasareserereres
                                                                                                                                                                                                                          CCAGGGAAGGGACTGGAATTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTAC
                                                                                                                                                                                                                                                                                                                                                      GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCCAGGGAGTCCTGGTCACCGTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-CD4 cynomolgus monkey immunoglobulin heavy chain variable region.
                                                                           Gaps
                                                                         ë
                                                    DB 14; Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-CD4 antibody; cynomolgus monkey; immunoglobulin; Ig. chimpanzee; chimeric antibody; human therapy; Old World
                                                                         68; Indels
                                 Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;
                                                   Score 298.2; DB 1-
Pred. No. 1.5e-67;
0; Mismatches 68
  immunological disorders. (Updated on 25-MAR-2003 to correct PN field.)
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/product= Anti-CD4_VH_region
/note= "No stop codon given"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antigen binding region; tumour; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT91564 standard; DNA; 423 BP
                                                    70.5%;
83.2%;
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91US-0735064
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                                                               Best Local Similarity 83.2
Matches 352; Conservative
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25-JUL-1991;
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Best Local S
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61 CTGCAGCTGCAGGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A new chimeric antibody (Ab) has been developed comprising a human or chimpanzee immunoglobulin (Ig) constant region and an Old World monkey antigen (Ag)-binding region. The present sequence encodes an anti-CD4 cynomolgus monkey Ig heavy chain variable region. An anti-CD4 antibody (Ab) comprising the light- and heavy-chain variable regions encoded by the present sequence and that of AAT91565 is also new. The Abs are useful for human therapy, especially of tumours. Old world monkeys are sufficiently different from humans to allow Abs against human Ags, even relatively conserved Ags such as CD4 and CD54, to be raised in these monkeys, and are sufficiently similar to humans to avoid host anti-Ab immune responses when the Abs are introduced into humans. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 AACCCGTCCCTCAAGAGTCGAGTCATTTCACAAGACACGTCCAAGAACCAGTTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                        antibodies for human therapy - comprising human or immunoglobulin constant region and an Old World monkey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                            chimpanzee immunoglobulin constant
antigen-binding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 33; Fig 13; 46pp; English.
                                                                                                                                                                                            Raab RW;
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83.2%;
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92US-0856281
95US-0379072
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Best Local Similarity 83.2
Matches 352; Conservative
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63

360

300

monkey; baboon; n: chimpanzee; hybrid;

360 420

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CTGAACCTGAACTCTGTGACCGCCGCGGACACGCCGTGTATTACTGTGCCAGAGATTGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Ig heavy chain variable region"
/note= "no stop codon given at the 3' end of sequence"
                 361 GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC
                                                                                                                                                                                                                                                                                                                    primer; PCR; amplification; leader sequence; human; monkey; baboon;
macaque; immunoglobulin; heavy chain variable region; chimpanzee; hyb
lymphoma; AIDS; autoimmune disease; inflammatory disease; transplant;
                                                                                                                                                                                                                                                                                               Monkey anti-CD4 heavy chain variable region coding sequence.
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4..420
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92US-0856281.
95US-0379072.
95US-0481869.
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                                                                                                                                                                                                                                                                                                                                                                  tumour; antibody; ss.
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                                                                                                                                                                                                             standard;
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07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This DNA encodes the heavy chain variable region (VH) of the cynomolgus monkey anti-CD4 antibody. The antibody comprises antigen-binding sequences from an Old World monkey antibody and human constant domain sequences. The antibody specifically binds to CD4 and can be used in the treatment of rheumatoid or psoriatic arthritis.
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                                                                                                                                                                                 transl_except= (pos:415..417, aa:Ser)
product= "Variable heavy chain antigen binding
                                                       Anti-CD4 antibody; antigen-binding; treatment; chimeric; human; monkey; rheumatoid arthritis; psoriatic arthritis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treatment of rheumatoid and psoriatic arthritis - comprises administration of chimeric human-monkey anti-CD4 antibody
                           Anti-CD4 antibody variable heavy (VH) region encoding DNA
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Pred. No. 1.5e-67;
0; Mismatches 68; Indels
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                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                              region"
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                                                                                                Chimeric - Macaca cynomolgus.
Chimeric - Homo sapiens.
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91US-0735064.
92US-0856281.
92US-0912292.
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 (first entry)
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Matches 352; Conservative
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10-AUG-1998
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10-JUL-1992
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This sequence represents the coding sequence for the heavy chain variable region from an anti-human CD4 immunoglobulin raised in cynomolgus monkeys. The sequence was PCR amplified and used in the construction of a recombinant antibody comprising: (i) an Old World monkey Ig antigen-binding region; and (ii) a human or chimpanzee Ig constant region. The hybrid antibodise can be used as passive or active therapeutic agents against human diseases, e.g. B-cell lymphoma, AIDS, autoimmune and inflammatory diseases, transplant rejection or Nucleic acid encoding hybrid antibody - comprising monkey antigen-binding region and human or chimp constant region

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tumours, or for producing therapeutic and diagnostic conjugates. Although evolutionary distant monkeys are used to raise antibodies against human antigens, they are sufficiently similar that they produce antibodies similar to human antibodies, such that when the monkey antibodies are introduced into humans, no host anti-antibody response
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                                                                                                                                                       Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;
                                                                                                                                                                                                                                             68;
                                                                                                                                                                                                70.5%; Score 298.2; DB 1
llarity 83.2%; Pred. No. 1.5e-67;
Conservative 0; Mismatches 68
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The invention describes a recombinant antibody comprising a human, chimpanzee or a first Old World monkey immunoglobulin constant region, and an antigen-binding portion of a second Old World monkey can be an antigen-binding portion of a second Old World monkey can be the same or different. The recombinant antibody is useful for treating a human having the antigen described above, e.g. for treating cancer in a human having the undurantigen, or for treating a human sutfering from an autoimmune response (where the antigen is involved in an autoimmune response in the human). In particular, the recombinant antibody is useful for treating rheumatoid arthritis, eczema, or an intrody is useful for treating themmatoid arthritis, eczema, or an treating tumours, leukaemia, lymphoma, Hashimoto's thyroiditis, autoimmune carditis, Addison's disease, type I-diabetes mellitus, autoimmune carditis, male infertility autoimmune hemolytic anaemia, inflammatory bowel disease, Sjogern's syndrome, psoriaeis, or systemic commingiobulin heavy variable chain polypeptide for creation of the
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                                                                                                                                                                                                                                                                                                                                                                                              New recombinant chimeric antibodies comprising human, chimpanzee and Old World monkey portions, useful for treating e.g. cancer, eczema, leukemia, lymphoma, Hashimoto's thyroiditis, multiple sclerosis or male
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Pred. No. 1.5e-67;
0; Mismatches 68; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an antibody to human CD40, or its functional fragment, has at least one of the following properties: acting on dendritic cells to produce IL-12 in the presence of LD8 (lipopolysaccharide) and irNgamma (interferon gamma); acting on dendritic cells to activate maturity of the dendritic cells with high GD8-5 antibody against antibody, and activating CD9s expression with high GD8-5 antibody against B cell line. Such antibodies or functional fragments can be used as immunoactivators, anti-tumour agents, immunosuppressants, and as remedies for autoimmune diseases, allergy or coagulation factor VIII inhibitors syndrome. This polymuclectide sequence represents a coding DNA sequence relating to the anti-CD40 monoclonal antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                       Antiallergic; haemostatic; immunomodulator; cytostatic; antibody; human CD40; IL-12; LPS; lipopolysaccharide; IFNgamma; interferon gamma; dendritic cell; high G28-5; B cell line; immunoactivator; atti-tumour agent; immunosuppressant; allergy; autoimmune disease; coagulation factor VIII inhibitor; anti-CD40; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD4( or functional fragment, is useful in the treatment of e.g. autolmmune
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                                                                                                                                                                                                                                                                                                                          Anti-CD40 monoclonal antibody related DNA SEQ ID No 43.
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84.6%; Pred. No. 4.1e-67;
ive 0; Mismatches 59
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                                                                                                                                                                           ABT31871 standard; DNA; 481 BP.
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11-MAY-2001; 2001UP-0147482.
05-OCT-2001; 2001UP-0310535.
26-OCT-2001; 2001US-0040244.
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TCA 423
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7

Gaps

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59; Indels

358; Conservative

Matches

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52 ATGAAACATCTGTGGTTCTTCCTTCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 111 CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAGGCCTTCGGAGACCCTGTCCCTCACC 120

61

1 ATGAAACACCTGTGGTTCTTCCTCCTCGTGGTGGCTCCCAGATGGGTCCTGTCCCAG

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229 CCAGGGAAGGGACTGGAGTGGATTGGGTATATCTATTACA---GTGGGAGCACCAACTAC 285
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                                                               112 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCTGTCCCTCACC 171
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                                                                                                                              CCAGGGAAGGGACTGGAGTTGGACGTATCTCTCTGGTAGTGGTGGGCCCACCAACTAC
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Job time : 185.558 secs
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Sequence 114, App Sequence 74, Appl Sequence 198, App Sequence 198, App Sequence 7, Appli Sequence 7, Appli Sequence 1, Appli Sequence 1, Appli

Sequence 2, Appli Sequence 110, App Sequence 106, App

Appli

Sequence 9

Appli Appli

Sequence Sequence

Sequence

Sequence 13, Appl Sequence 21201, A Sequence 1375, Ap Sequence 16650, A

Appli Appli Appl

Sequence 210, App Sequence 4, Appli

4, Appli 1, Appli 13582, A 114467,

Sequence 1 Sequence 1

Sequence 4, Sequence 4, Sequence 43,

Sequence 114467, Sequence 114467,

OM nucleic

Run on:

Sequence:

Searched:

Database

Š Š Result

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KLOETZER, William S.
NAKAMURA, TAKENİKO.
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL.
ANTIBODIES AND USE THEREOF AS THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
STREET: P.O. Box 1404
CITY: Alexandria
STRATE: Virginia
COUNTRY: United States
ZIE: 2213-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,441
FILING DATE: 05-Feb-1998
CLASSIFICATION: AURHOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-920-345-4
US-10-182-132-1
US-10-198-846-13582
US-10-027-632-114467
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-502
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1936-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09019441 Publication No. US20030086921A1 GENERAL INFORMATION: REFF, Mitchell E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            836-2021
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INFORMATION FOR SEQ ID NO: 2:
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264.2
262.6
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2371.523 Million cell updates/sec
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                                                                                                                                                                      ; Search time 611.125 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2,
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1 ATGAAACACCTGTGGTTCTT.....TCCTGGTCACCGTCTCCTCA
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1: \cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: \cgn2_6/ptodata/2/pubpna/PCT_MEW_PUB.seq:*
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17: \cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
18: \cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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18: \cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                             GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
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US-10-103-686-2
US-10-124-807-11
US-10-291-532-11
US-10-291-532-11
US-10-291-532-11
US-09-905-243-40
US-09-905-243-40
US-10-211-357-9
US-10-211-357-9
US-10-211-357-9
US-10-211-357-9
US-10-211-357-9
US-10-211-357-9
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US-10-211-357-1
US-10-300-675-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lotal number of hits satisfying chosen parameters:
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                                                                                                                                                                      December 29, 2003, 19:01:43
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                         nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match 1
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Perfect score:
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NAME: TERLIN, RODIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
TELECOMMUICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-2021
                                           APPLICATION NUMBER: US/10/103,686
FILING DATE: 25-Mar-2002
CLASSIPICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
            SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3
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SEQUENCE DESCRIPTION: SEQ ID NO: US-10-103-686-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 11, Application US/09948429B ; Patent No. US20020177689A1
                                                                                                                                                                                                                                                                                                           LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
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58..423
                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
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US-09-948-429B-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
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Best Local
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                                                                                                                                                                                                                                                              Length 423;
                                                                                                                                                                                                                                                                                              Indels
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CORRESPONDENCE ADDRESS:
ADDRESSES: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUWRY: United States
ZIP: Z2313-1404
                                                                                                                                                                                                                                                            Score 423; DB 11;
Fred. No. 2.3e-116;
Mismatches 0;
                                                                                                                                                                                           LOCATION: 58.7423
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Publication No. US20030059424A1
GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
NAKAMURA, Takehiko
                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                       NAME/KEY: mat_peptide
LOCATION: 58..423
              LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                              100.0%;
SEQUENCE CHARACTERISTICS:
                                                                                                                                        1..423
                                                                                                                                                                                                                                                                                                423; Conservative
                                                                                                                       NAME/KEY:
                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                              Similarity
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US-10-103-686-2
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Best Local
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Version #1.30
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100.0%; Pred. No. 2.3e-116;
tive 0; Mismatches 0;
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240 240

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GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                        405
301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGATTGG 360
                                                                  301 creaagcreaacrerareaccecececeacacececererarracrerereaeaacacer 360
                                                                                                                                                                                                           361 CTTTTTCAGTTGTTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGGAGTC 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 74.0%; Score 313.2; DB 1:
Best Local Similarity 84.5%; Pred. No. 1.6e-83;
Matches 370; Conservative 0; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PREDEIGTION NUMBER: 09/383,916
FILING DATE: 07-UNH-1995
FILING DATE: 07-UNH-1995
ATTORNEY/AGENT INFORWATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/10124807
Publication No. US20030166207A1
                                                                                                                                                361 GCCCAAATAGCTGGAACAA----
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STRANDEDNESS: not relevant
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                        406 CTGGTCACCGTCTCCTCA
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, LOCATION:
US-10-124-807-11
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              "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
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Pred. No. 1.6e-83;
0; Mismatches 53; 1
                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
FILING DATE:
                                 TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBOD TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS TITLE OF INVENTION: IMMUNOSUPPRESANTS" NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     012712-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
   Darrell R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012
TELECOMMUNICATION: TELEPHONE: 703-836-6620
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IYPE: nucleic acid
STRANDEDNESS: not relevant
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Best Local Similarity 84.5%;
Matches 370; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
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US-10-291-532-11

i Sequence 11, Application US/10291532

i Bequence 11, Application US/10291532

i Bequence 11, Application Wo. US20030180290A1

i GENERAL INFORMATION:

APPLICANT: HARNA, KANDASAMY

APPLICANT: HARNA, NABIL

ITILE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC

ITILE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC

ITILE OF INVENTION: COMBINATION WITH OTHER THERAPIES

FILE REFERENCE: 037003/29187

CURRENT APPLICATION NUMBER: US/10/291,532

CURRENT APPLICATION NUMBER: 08/31,187

PRIOR FILING DATE: 2001-11-09

PRIOR FILING DATE: 2001-01-12

PRIOR PELING DATE: 1999-08-26

PRIOR FILING DATE: 1999-08-26

PRIOR FILING DATE: 1995-06-07

NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                          AACCCGTCCATCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
                                                                                                                                                                                                                                                                                                   CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGATTGG 360
                                                                             GTGCAGCTGCAGGAGTCGGGCCCCAGGACTGGTGAAGCCTTCGGAGACCTTGGTGTCCCTCACC 120
                                                                                                                               TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC 180
                                                                                                                                                      CCAGGGAAGGGACTGGAGTTGGACGTATCTCTCTGGTAGTGGTGGGGCCCACCAACTAC 240
                                                                                                                                                                                                                                     ccadegaaggggcregagregarreggagrreraragragregaggagacrecracrac 240
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                                                       CTGCAGCTGCAGGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: primatized nucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
74.0%; Score 313.2; DB 13; Length
Best Local Similarity 84.5%; Pred. No. 1.6e-83;
Matches 370; Conservative 0; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          credricaccercrica 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGTCACCGTCTCCTCA
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SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) NAME/KEY: CDS
; LOCATION: (1)..(1428)
US-10-291-532-11
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1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG

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Sequence 11, Application US/10124905
Publication No. US20020166136A1
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSED:
BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CORRESPONDENCES:
CORR
                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                                                                                                      121 TGCGCTGTCTCTCGCGCTCCATCAGCGGTGGTTATGGCTGGGCTGGATCCGCCAGCCC 180
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1 ATGAAACACCTGTGGTTCTTCCTCCTCGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
                                                                                                                                                                                       61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,905
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REPERENCE/DOCKET NUMBER: 012712-131
TELEFOWNINICATION INFORMATION:
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
COURSE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 CTGAAGCTGAACTCTATGACCGCCGCGGACACGGCCGTGTATTACTGTGTGAGAGTCGT 360
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TITLE OF INVENTION: Monoclonal Antibodies with Reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.0%; Score 313.2; DB 1
84.5%; Pred. No. 1.6e-83;
iive 0; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                     APPLICATION NUMBER: US/10/073,138
FILING DATE: 13-Feb-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                             APPLICATION NUMBER: US/08/746,361
FILING DATE: 08-NOV-1996
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1..1431
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 GCCCAAATAGCTGGAACAA-----
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.sequence 40, Application US/09905243
.petent No. US20020062009A1
.general information:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1431 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
CURRENT APPLICATION DATA:
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                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 370; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACCCGTCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 AACCCCTCCTCAAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTCTCC 300
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BRAMS, Peter
TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 313.2; DB 14;
Pred. No. 1.6e-83;
0; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/10073138
Publication No. US20020187146A1
GENERAL INFORMATION:
APPLICANT: ANDERSON, Darrell R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 GCCCAAATAGCTGGAACAA----
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CITY: Alexandria
STATE: Virginia
COUNTRY: United States
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                                                   not relevant
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Best Local Similarity 84.5%;
Matches 370; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, I
                                                                                                                                                                                                                                                                                                                                                              mat_peptide
                                STRANDEDNESS: not rel
TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:

LOCATION:

US-10-124-905-11
                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                     LOCATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, '
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/211,357
                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
POSITION IN GENOME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
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Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
Therapy
                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                           Length 423;
                                                                                                                                                                                                                                                                                                                                                                               58; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
CUNTKY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                         71.2%; Score 301.2; DB 9;
85.0%; Pred. No. 5e-80;
                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
  TITLE OF INVENTION: Immunogenicity
FILE REFERENCE: P50770
CURRENT APPLICATION NUMBER: US/09/905,243
FURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/300,970
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/10211357
Publication No. US20030077275A1
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Macaca cynomolgus
                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 85.0 Matches 362; Conservative
                                                                                                                                                                                                                                                                                  ... (423)
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                                                                                                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (1)
US-09-905-243-40
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US-10-211-357-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 70.9%; Score 299.8; DB 15; Length 1404; Best Local Similarity 83.5%; Pred. No. 1.6e-79; Matches 353; Conservative 0; Mismatches 67; Indels 3;
Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
                                                                                               FILING DATE: 05-Aug-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/612,914A
                                                                                                                                                                                                                                      FILING DATE: 10-Jul-2000
APPLICATION NUMBER: US 08/523,894
FILING DATE: 06-SEP-1995
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TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1404 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 703-836-2021 INFORMATION FOR SEQ ID NO: 11:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/102
Publication No. US20030077275AL
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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                                                                                                                                                                  Newman, Roland A.
Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
Therapy
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                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
CONDITY: USA
CONDITY: USA
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BATERIN: PC-DOS/MS-DOS
SOFTWARE: PATERIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 05-Aug-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 299.8; DB 15; Length
Pred. No. 1.6e-79;
0; Mismatches 67; Indels
                                                                                                                                                                                                                                                                               SWECKER & MATHIS
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APPLICATION NUMBER: US/09/612,914A
PILIG DATE: 10-Jul-2000
APPLICATION NUMBER: US 08/523,894
FILING DATE: 06-SEP-195
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35,030
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, STREET: 699 Prince Street
                                                                                         Sequence 9, Application US/10211357
Publication No. US20030077275A1
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 83.5%;
Matches 353; Conservative C
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LOCATION:
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418 TCA 420
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US-10-211-357-9
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TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGAACCTGGATCCGCCAGCCC 180
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Reff, Mitchell B.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/10/211,357
FILING DATE: 05-Aug-2002
CIASSIFICATION: CURROWN>
PRIOR APPLICATION UNMBER: US/09/612,914A
FILING DATE: 10-Jul-2000
APPLICATION NUMBER: US 08/523,894
FILING DATE: 06-SEP-1995
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSER: BURNS, DOANE, STREET: 699 Prince Street
CITY: Alexandria
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Sequence 15, Application US/09850165; Patent No. US20020150580A1
GENERAL INFORMATION:
           70.5%;
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             Query Match
Best Local Similarity 83.23
Matches 352; Conservative
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                                                                                                                                                                                                                                                                     Gaps
           POSITION IN GENOME:
CHROMOSOME/SEGMENT: heavy chain gamma 4 with the P and
mutation
                                                                                                                                                                                                                                   DB 15; Length 1404;
                                                                                                                                                                                                                                 Query Match 70.9%; Score 299.8; DB 15; Length Best Local Similarity 83.5%; Pred. No. 1.6e-79; Matches 353; Conservative 0; Mismatches 67; Indels
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US-09-905-243-44
; Sequence 44, Application US/09905243
; Patent No. US-0020062009A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; TITLE OF INVENTION: MONOCLONAL AND APPLICATION WIMBER: US/09/905,243
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/300,970
; PRIOR PILING DATE: 1999-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 44
LENGTH: 420
                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                          mat_peptide
ORGANISM: Homo sapiens
                                                                                                          1..1404
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CRGANISM: Macaca cynomolgus
FRATURE:
NAME/KEY: CDS
LOCATION: (1)...(420)
US-09-905-243-44
                                                                     FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                          NAME/KEY:
LOCATION:
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                                                                                                                           FEATURE
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61 CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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                                                                                                                                                                     1 ATGAAGCACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGCTCCCAG
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APPLICANT: HANNA, NABIL
APPLICANT: HANNA, NABIL
TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
FILE REFERENCE: 037003-0280614
CURRENT PAPLICATION NUMBER: US/09/850,165
CURRENT PILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: 09/082,472
PRIOR APPLICATION NUMBER: 09/082,472
PRIOR APPLICATION NUMBER: 08/476,237
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR PLING DATE: 1992-03-3
PRIOR PLING DATE: 1992-03-3
PRIOR PLING DATE: 1992-07-10
PRIOR PLING DATE: 1992-07-10
PRIOR PLING DATE: 1992-07-10
PRIOR PLING DATE: 1992-07-10
PRIOR PLING DATE: 1992-07-11
Length 420;
                                                        Indele
   DB 9;
   Score 298.2; DB 9 Pred. No. 3.9e-79
                                                        0; Mismatches
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LOCATION: 61.720
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                         35,030
                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: MONKEY
                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 420 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                mat_peptide
                                                                                                    TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.8%;
83.1%;
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Best Local Similarity 83.1
Matches 349; Conservative
                                                                                                                                                                                                                                                                                                      POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                              FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 420
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                                                                                                                                                                                  4 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCCCCCAGATGGGTCTTGTCCCAG 63
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Newman, Roland A.
Reff, Mitchell B.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
Therapy
                                                                                                    <u>ب</u>
                                                                                                                                          1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGT
                                                               Length
                                                                                                  68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWECKER & MATHIS
                                                            DB 10;
                                                      Score 298.2; DB 1
Pred. No. 3.9e-79;
0; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/612,914A
FILING DATE: 10-011.2000
APPLICATION NUMBER: US 08/523,894
FILING DATE: 06-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/211,357
FILING DATE: 05-Aug-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSER: BURNS, DOANE, STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10211357
Publication No. US20030077275A1
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION
                                                      70.5%;
83.2%;
                                                                                                Matches 352; Conservative
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; LOCATION: (4)..(420)
US-09-850-165-15
                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCA 423
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                                                          Query Match
Best Local 8
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304 CTGAAACTGAGGTCTGTGACCGCCGCGCGCACACGGCCGTCTATTACTGTGCGAGTAAT--- 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHROMOSOME/SEGMENT: light variable domain of CE9.1
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APPLICANT: Watkino.

TITLE OF INVENTION: Tumor Specific Monoclonal Antibodies; FILE REFERENCE: P-IX 5519; CURRENT APPLICATION NUMBER: US/10/300,675; CURRENT FILING DATE: 2002-11-19; PRIOR APPLICATION NUMBER: US 09/989,901; PRIOR FILING DATE: 2001-11-19; NUMBER OF SEQ ID NOS: 59; NUMBER OF SEQ ID NOS: 59; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Pred. No. 3.1e-78;
0; Mismatches 68;
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
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120

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300

240

360

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155 GCAGCTCGTCCTCACCGATACTTTGACTACTGGGGCCAGGGAACCCTGGTCACGCTCTCC 414
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                                                                                                                                          Gaps
                                                                                                               Query Match

69.4%; Score 293.4; DB 13; Length 417;
Best Local Similarity 84.2%; Pred. No. 1.1e-77;
Matches 356; Conservative 0; Mismatches 61; Indels 6;
; SEQ ID NO 1
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FRATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (417)
US-10-300-675-1
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Search completed: December 30, 2003, 03:42:09 Job time: 613.125 secs

55, Appl 4, Appli 61, Appl 4, Appli

Appli

Sequence Sequence Sequence

Sequence

Appli Appli Appli Appli Appli

Sequence 9, Ag Sequence 59, A Sequence 7, Ag Sequence 31, A

App]

Sequence Sequence Sequence Sequence Sequence

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

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GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
APPLICANT: KLOETER, William S.
APPLICANT: KLOETER, William S.
APPLICANT: NAKAWURA, Takehiko
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 423; DB 3; Length 423;
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CONDUTRY: United States

CONDUTRY: United States

COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35.03
REFERENCE/DOCKET NUMBER: 35.03
RELEPAX: (703) 836-6620
TELEPHONE: (703) 836-2021
INFORMATION POR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                           US-08-468-671-5
US-08-545-809A-55
US-09-260-52A-4
US-08-545-809A-41
US-08-545-809A-39
US-08-360-125-9
US-08-450-578-9
US-09-017-628-9
 .08-758-417A-199
                -09-582-337-13
-08-545-809A-28
-08-259-372A-5
                                                                                                                                                                                                                                    -08-545-809A-59
-08-793-450-7
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TYPE: nucleic acid
STRANDEDNESS: single
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US-08-803-085-2
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                                                                                                           December 29, 2003, 16:08:50 ; Search time 46.5619 Seconds (without alignments) 4009.823 Million cell updates/sec
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                                                                                                                                                                                                          1 ATGAAACACCTGTGGTTCTT......TCCTGGTCACCGTCTCCTCA 423
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-523-894-9
US-08-523-894-9
US-08-478-011
US-08-478-037-105
US-08-478-037-107
US-08-478-037-107
US-08-478-037-107
US-08-478-037-107
US-08-526-098-3
US-09-526-098-3
US-09-626-098-3
US-09-042-353-357
US-09-042-353-357
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US-09-372-425A-1
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US-09-042-353-351
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Maximum Match 100%
Listing first 45 summaries
                                                                               - nucleic search, using sw model
                                                                                                                                                                                                                                         IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Issued_Patents_NA:*
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Maximum DB seq length: 200000000
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Match Length DB
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Score

Result 8 2566.2 266.2 266.2 263.8 261.2 261.2 257.8 257.8 257.8

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CTGGTCACCGTCTCCTCA 438
nucleic acid
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Best Local Similarity 84.5%;
Matches 370; Conservative
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                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ADDRESSEE: BURNS, DC
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CITY: Alexandria
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              STRANDEDNESS
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, LOCATION:
US-08-487-550-11
                                                                                      NAME/KEY:
                                                                                                      LOCATION:
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Patent No. 6113898
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF AS
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPRESANTS"
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BUBNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCCAAATAGCTGGAACAACGCTTCTGGGGCCAGGAATCCTGGTCACCGTCTCC 420
                                                                                                                        CTGCAGCTGCAGGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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                                                                                                                                                        CTGCAGCTGCAGGAGTCGCGCCCAGGAGTGATGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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                   Gaps
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BY SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
SOFTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
   6.7e-114;
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 100.0%; Pred. No. 6. ive 0; Mismatches
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REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEPHONE: 703-836-6220
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
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                                                                                                                                                 Gaps
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Length 1431;
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       DB 3;
Score 313.2; DB 3
Pred. No. 8.7e-82;
0; Mismatches 53
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699 Prince Street
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Sequence 11, Application US/09526098
Patent No. 6492134
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
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61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCTCACC 120
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                                        APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUECES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heavy chain variable and constant gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FLING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: TESKION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 012712-165
TELEPHONE: 700-86-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 299.8; DB 3;
Pred. No. 6.8e-78;
0; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
POSITION IN GENOME:
Newman, Roland A. Reff, Mitchell E.
                                                                                                                                                                                                                                                                                   ADDRESSEE: BURNS, DOANE, STREET: 699 Prince Street CITY: Alexandria
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Best Local Similarity 83.5%;
Matches 353; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CHROMOSOME/SEGMENT:
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LOCATION:
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LOCATION:
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                                                                                                                                                                                                                                     FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX:
     US/09/526,098
                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
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Patent No. 6136310
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
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Matches 370; Conservative
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MOLECULE TYPE: peptide
     APPLICATION NUMBER:
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                                                                                                     CLASSIFICATION:
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LOCATION:
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, LOCATION:
US-09-526-098-11
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TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                           361 GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
TITLE OF INVENTION: Therapy
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STREET: USA
COMPTRY: USA
COMPTRY: READABLE FORM:
MEDIUM TYPER: Floppy disk
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER TEADABLE FORM:
COMPUTER T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHROMOSOME/SEGMENT: heavy chain gamma 4 with the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/523,894 FILING DATE: U6-SEP-1995 CLASSIFICATION: 424 ATTONREY/AGENT INPOMMATION: NAME: TEAERIOR NUMBER: 35,030 REFERENCE/DOCKET NUMBER: 35,030 REFERENCE/DOCKET NUMBER: 35,030 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEFRAX: 703-836-6620
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83.5%;
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TYPE: nucleic acid
STRANDEDNESS: single
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POSITION IN GENOME:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 353; Conservative
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MOLECULE TYPE: I
ORIGINAL SOURCE:
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LOCATION:
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US-08-523-894-9
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APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell B.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHROMOSOME/SEGMENT: heavy chain gamma 4 with the P CHROMOSOME/SEGMENT: mutation
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTONREY/AGENT INFORMATION:
NAME: TESEKIN, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
TELEPROMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 699 Prince Street CITY: Alexandria STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPAtible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08523894 Patent No. 6136310
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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FILING DATE:
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Sequence 19, Application US/08379072A
Fatent No. 5658570
GENERAL INFORMATION
APPLICANT: HANNA, Nabil
APPLICANT: HANNA, Nabil
APPLICANT: RAAB, Ronald W.
TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia States
COUNTRY: United States
                                                                                                                                                                       3;
                                                                                                                                       Length 1404;
                                                                                                                                                                       67; Indels
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APPLICATION NUMBER: US/08/379,072A FILING DATE: 25-JAN-1995 CLASSIFICATION: 424
                                                                                                                                     Score 299.8; DB 3;
Pred. No. 6.8e-78;
                                                                                                                                                                       0; Mismatches
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APPLICATION NUMBER: US 07/912,292
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                   70.9%;
83.5%;
                                                                                                                                                       Best Local Similarity 83.5
Matches 353; Conservative
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                NAME/KEY:
LOCATION:
FEATURE:
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                                                                 ), NAME/KEY:
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US-08-523-894-11
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181 CCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTAC 240
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CENERAL INPORMATION:
APPLICANT: HANNA, Roland A.
APPLICANT: RAAB, Ronald W.
TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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P.O. Box 1404
                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-UU-1991
ATTORNY AGENT INFORMATION:
NAME: Rea, Teresa Stanek
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 012712-067
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-620
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                    UMBER: US 07/856,281
23-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
US-08-379-072A-19
10-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                          PRIOR APPLICATION DATA
APPLICATION NUMBER:
FILING DATE: 23-MAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 352; Conserv
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241 AACCCGTCCTCAAGAGTCGAGTCATTTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
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                                                                                                                                                                                                                         APPLICANT: NEWMAN, Roland A.
APPLICANT: HANNA, Nabil
APPLICANT: RAAB, ROMANDI W.
TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 423;
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COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,237
FILING DATE: 07-JUN-1995
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION NUMBER: US 07/735,064
ATPLICATION NUMBER: US 07/735,064
ATPLICATION NUMBER: US 07/735,064
ATPLICATION NUMBER: US 07/735,064
ATPLICATION NUMBER: DS 07/735,064
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70.5%; Score 298.2; DB:
Best Local Similarity 83.2%; Pred. No: 1.3e-77
Matches 352; Conservative 0; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REGISTRANCE/DOCKET NUMBER: 012712-133
TELECOMMUNICATION INPORMATION:
TELEPHONE: (703) 836-6620
                                                                                                              US-08-476-237-15
; Sequence 15, Application US/08476237
; Patent No. 5756096
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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EDNESS: single
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ADDRESSEE: Burns, Do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
TCA 423
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                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
COMPUTER: PIOPPy disk
COMPUTER: PIOPPy disk
COMPUTER: PE PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,869
FILING DATE:
CLASSIFICATION: S36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/39,072A
FILING DATE: 25-401-1992
PRIOR APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-401-1992
PRIOR APPLICATION NUMBER: US 07/912,292
FILING DATE: 23-MAR-1992
PRIOR APPLICATION NUMBER: US 07/912,092
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 23-MAR-1992
PRIOR APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-401-1991
ATTORNEY/AGENT INPORMATION:
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Pred. No. 1.3e-77;
0; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Rea, Teresa Stanek
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 012712-067
TELECAMUNICATION INFORMATION:
TELEPHONE: (703) 836-620
TELEPHONE: (703) 836-2021
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 Asse pairs
LENGTH: 423 Asse pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
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  : Virginia
RY: United States
22313-1404
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Best Local Similarity 83.2
Matches 352; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 CCAGGGAAGGGACTGGAGTGGATCGGCTACATCTATGGCAGTGGTGGGGGCACCAATTAC 243
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                                                                                                                                                                                                                                                                                            4 ATGAAACACCTGTGGGTTCTTCCTCCTCCTGGTGGCAGCCCCCAGATGGGTCTTGTCCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 IGCAGIGICICIGGIGGCICCAICAGCGGIGACIATIATIGGIICIGGAICCGCCAGICC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 AACCCGTCCTCAAGAGTCGAGTCATTTCACAAGACACGTCCAAGAACCAGTTCTCC
                                                                                                                                                                                                                                                                 1 ATGAMACACCTGTGGTTCTTCCTCCTCCTGGTGGCTCCCAGATGGGTCCTGTCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 GCCCAAAIAGCTGGAACAACGCTAGGCTICTGGGGCCAGGGAGTCCTGGTCACCGTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
CORRESPONDENCE: 114
                                                                                                                                                                   Length 420;
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA

ZIP: 2213-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,349A
                                                                                                                                                                   DB 1;
                                                                                                                                                              Score 295.2; DB .
Pred. No. 9.8e-77
0; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGT
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I: 699 Prince St.
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ν. ν. υς/08/476,349Α
07-JUN-1995
N: 514
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APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 107, Application US/08476349A
Patent No. 5750105
GENERAL INFORMATION:
                                                                                                                                                                69.8%;
83.1%;
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Matches 349; Conservative
                                                                     mat_peptide
61..420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                      ; FEATURE:
; NAME/KEY: "
; LOCATION: 6
; LOCATION: 6
US-08-478-039-107
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US-08-476-349A-107
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  NAME/KEY:
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STATE:
                                                                                                                                                                        Query Match
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                                                                                                                    304 crcanacrdacrcrcrcrcrccccccccccccccrrrrrrrrcrcrcraran--- 360
                                                                                                                                                                   361 GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 420
                        244 AATCCCTCCCTCAACAATCGAGTCTCCATTTCAATAGACACGTCCAAGAACCTCTTCTCC 303
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/912,292
FILING DATE: 13-MAR-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/35,064
FILING DATE: 25-JAN-1992
RAPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN ESQ., RODIN L.

REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 107, Application US/08478039; Patent No. 5681722; GENERAL INFORMATION: APPLICANT: Newman, Roland A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Anti-CD4 VH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: not relevant
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 base pairs
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Alexandria
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TCA 423
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ORIGINAL SOURCE:
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US-08-478-039-107
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TITLE OF INVENTION: Th
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DO
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LOCATION:
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                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 420
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Patent No. 6135310
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 420;
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83.1%; Pred. No. 9.8e-77;
iive 0; Mismatches 68
APPLICATION NUMBER: US 07/856,281
FILING DATE: 33-MAR-1992
PRIOR APPLICATION DATA: 400
FILING DATE: 25-UJU-1991
ATTONNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEPHONE: 703-836-2021
INFORMATION FOR SEQ 1D NO: 107: 5000ENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHROMOSOME/SEGMENT: Anti-CD4 VH
                                                                                                                                                                                                                                                                                                                                                                                  STRANDENNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                        LENGTH: 420 base pairs
TYPE: nucleic acid
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Matches 349; Conservative
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US-08-476-349A-107
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LOCATION:
FEATURE:
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                                                                                                                                                                                              COMPUTER: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FLING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, Robin L.
REGISTRATION NUMBER: 35.030
REFERENCE/CONCET NUMBER: 012712-165
TELECOMMULCATION INFORMATION:
TELEFANCE 703-836-6620
TELEFAN: 703-836-6201
TELEFAN: 703-836-6201
TELEFAN: FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
69.8%; Score 295.2; DB 3
Best Local Similarity 83.1%; Pred. No. 9.8e-77,
Matches 349; Conservative 0; Mismatches 68
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 420 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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61..420
                                                                                                                                            ZIP: 22314-3187
COMPUTER READABLE FORM:
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APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCIONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                 405
                                                                                                                                         301 CTGAACCTGAACTCTGTGACCGCCGCGCGCACACGGCCGTGTATTACTGTGCCAGAGATTGG 360
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   241 AACCCGTCCACAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
                                                          241 AATCCCTCCCTCAAGAGTCGAGTCACATTTCAAAAGACACGTCCAAGAACCAGGTCTTC
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
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Pred. No. 9.7e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIPTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-UNN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01271
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09526098
Patent No. 6492134
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                          406 CTGGTCACCGTCTCCTCA 423
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TYPE: nucleic acid
STRANDEDNESS: not relevant
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Best Local Similarity
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LOCATION:
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, LOCATION:
US-09-526-098-3
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                                                                                                                                                                                                                                                                                                                Anderson, Darrell R.
VENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
VENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
VENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGGGAGGGGACTGGAGTGGGATTGGCCATATTTATGGTAATGGTGCGACCACCAACTAC 240
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361 ATATTGAAATATCTTCACTGGTTATTATACTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/POCKET UNBER: 35,030
TELECOMMULICATION INFORMATION:
TELECOMMULICATION: TO 2936 6620
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Pred. No. 9.7e-76;
0; Mismatches 66;
                                                                                                                                                                                                                                                                                                             APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONCLONAL ANTIBOD
TITLE OF INVENTION: "PO HUMAN B'.1 AND/OR B'.2
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                 US-08-487-550-3
; Sequence 3, Application US/08487550
Patent No. 6113898
; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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TELEPHONE: 703-836-2021
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Best Local Similarity
Matches 357; Conserva
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LOCATION:
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LOCATION:
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    Gaps
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APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Buughn, Mariah R.
TITLE OF INVENTION: HIWAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
    15;
66; Indels
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OPERATING SYSTEM: DOS
SOFTWARE: F881SEQ for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
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    0; Mismatches
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REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
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Patent No. 6135941
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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        Matches 357; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEREWITH
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US-09-049-672A-17
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                                                                                                                                                                                                                                                                                                              DB 3;
                                                                                                                                                                                                                                                                                                          Score 289.6; DB 3
Pred. No. 6.5e-75;
0; Mismatches 49
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                                                                           INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                              68.5%;
85.9%;
                   TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
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; CLONE: 1513264
US-09-049-672A-17
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Matches 371; Conserv
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; Search time 1603.14 Seconds (without alignments) 9875.644 Million cell updates/sec
                                                                                                                                                     US-09-019-441-3
387
1 ATGGACATGAGGTCCCCGC......GGACCAAGGTGGAATCAAA 387
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                               2888711 segs, 20454813386 residues
                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                           December 29, 2003, 16:08:50
                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                    IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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                                                                                           Run on:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

					SUMMARIES		
Result No.	Score	% Query Match	Length	03	ΙD	Des	Description
	-						
-	m	100.0	904	φ.	BD075127	BD07	5127 Met
7	42.	88.4	2	σ	HUMIGKW	M740	B HOMO B
e	42.	88.4	729		BD090625	BDO	$\sim$
4	42.	88.4	729		E40896	E408	96 Humaniz
ß	40.	88.0	388		HSA548508	AJ548	000 Homo
9	34.	86.4	390		MMU57571	US7	. Macaca
7	34.	86.4	396		E12918	E12918	Human mR
<b>œ</b>	34.	86.4	438		BD015544	BDO	44 Human
0	334.2	86.4	438		BD094922	BD094	CD.
10	32.	85.9	406		HUMIGKFAN	M8747	Human r
11	31.	85.6	400		AF228327	AF228	Homo
12	33	85.5	962		BC034141	BCO	
13	30	85.5	432		HUMIGKVCA	L01	es out
14	29	85.1	390		MMU57579	US7	579 Macaca mu
15	29	85.1	974		AX305000	AX3	
16	29	85.1	974		AX306529	AX3	
17	29	85.1	974		BD131246	BD1	
18	28		370		HSIGKLV20	X72	441 H. sapiens
10	26		396		HSPBLIGVD	227	
20	26		714		AX616570	AX6	AX616570 Sequence
21	25		383		HSIGKLV56	X72	sapi
22	24		430		AF417853	AF4	
23	324.6	83.9	448		BD182345	. BD1	BD182345 Anti CD
24	23		389		HSIGKLV06	X72	427 H.sapiens
25	ľ		728		AX327729	AX3	
26	323		728		BD182353	BD1	82353 Anti CD
27	~		388		HSTROIGVJ	X85	997 H.sapiens
28	_		390		HSFOGIL	X64	163 H.sapiens
29	_		441		HSU43767	U43	
30	$\overline{}$		- 716		AX327727	AX3	
31	_		650		HSA010446	AJO	
32	319.4		399		N	X72	X72444 H.sapiens
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34	œ		388		BD096602	BDO	
35	œ		926		BC029444	aCO	129444 Homo sapi
36	ന		390		HSU43773	U43	
37	14	81.3	369		HSIGKLV02	X72	sapi
38	2		395		HSIGKLV41	X72	
36	13		388		HSDELIGVJ	X82	
40	23		388		HSTREIGVJ	X85	sapie
41	3		427		BD182339	BD1	Anti
42	13		427		BD182341	BD1	32341 Anti
43	313,4	81.0	953		BC005332	BCO	05332
44	۳.		388		HSIGKLV58	X72	479 H. sapie

## ALIGNMENTS

102		-
BD075127 Method for integrating genes at specific sites in mammalian cells via homologous recombination and vectors for accomplishing the same.		1 (bases 1 to 19040) Reff,M.E., Barnett,R.S. and Mclachlan,K.R. Method for integrating genes at specific sites in mammalian cells
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19040 by DNA linear PAT 27-AUG- Method for integrating genes at specific sites in mammalian celvia homologous recombination and vectors for accomplishing the same.		татте
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BD075127 Method fo via homosame.	BD075127 BD075127.1 GI:22620730 JP 201516221-A/3. unidentified unidentified unclassified.	<pre>1 (bases 1 to 19040) Reff,M.E., Barnett,R. Method for integratin</pre>
27 27	NICON	NCE IORS
RESULT 1 BD075127 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE
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                                          429 bp mRNA linear PRI 04-MAY-2000
Homo sapiens immunoglobulin light chain variable region (IGL@)
M74019
via homologous recombination and vectors for accomplishing the same
Patent: JP 2001516221-A 3 25-SEP-2001;
IDEC PHARMACEUTICALS CORP
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    19040
    organism='Unidentified'

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/organism="unidentified"
/mol_type="genomic DNA"
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JP 2001516221-A/3
25-SEP-2001
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387; Conservative
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Best Local 8
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Homo sapiens Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

M74019.1 GI:186042

VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

ACCESSION

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 429)
Silbersteini, L.B., Jefferies, L.C., Goldman, J., Friedman, D.,
Moore, J.S., Nowell, P.C., Roelcke, D., Fruzanski, W., Roudier, J. and
Silverman, G.J.
Variable region gene analysis of pathologic human autoantibodies to
the related I and I red blood cell antigens
Blood (1991) In press
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon start=1
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CRASQSISSYINWYQQKPGKAPKILIYAASSLQSGVPSRFSGGGGGTDFTLTISSLQP
EDPATYYCQQSYSTPWTFGQGTKVEIKRTVAAPSVFIFPPS"
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/gene="IGL@"
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Togo by DNA 11

Drug containing humanized anti-Fas antibody.

BD090625

BD090625.1 GI:22636235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 342.2; DB 9;
Pred. No. 5.9e-101;
0; Mismatches 28;
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/chromosome="22"
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67. .429
/gene="IGL@"
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Best Local Similarity 92.8%;
Matches 359; Conservative 0
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/gene="IGL@"
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KEYWORDS

COMMENT

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Homo sapiens partial mRNA for immunoglobulin light chain variable region (IGLV gene), clone RN86.
AJ548508.
IGLV gene; immunoglobulin light chain variable region.
Homo sapiens (human)
                                                                                                                                                                                                                                                       NOBUKI SERIZAWA,HIDEYUKI HARUYAMA,KAORI NAKAHARA,IKUKO TAMAKI CI2N15/09,A61K39/00,A61K39/395,A61K39/395,A61P37/02,A61P43/00,C07K16/18,C12N1/21,C12N5/10,C12P21/08//(C12N1/21,C12R1:19),C12N15/00,PC
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                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Granawa, N.; Haruyama, H.; Nakahara, K. and Tamaki, I.

Humanized anti-Fas antibody
Patent: 10 2000166574-A 85 20-JUN-2000;

SANKYO CD LTD

OS Homo sapiens (human)

PN JP 2000166574-A/85

PD 20-JUN-2000

PP 29-SEP-1999 JP 1999275441
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    .729
    /organism='Homo sapiens (human)'.

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Pred. No. 6.1e-101;
0; Mismatches 28;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
| 200 c 182 g 159
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Best Local Similarity 92.8%;
Matches 359; Conservative 0
sapiens (human)
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                                                     Eukaryotani
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (basea 1 to 729)
Serizawa,N., Haruyama,H., Nakahara,K. and Tamaki,I.
Drug containing humanized anti-Fas antibody
Patene: JP 2001342148-A 85 11-DEC-2001;
SANKYO CO LID
OS Homo sapiens (human)
Dr JP 2001342148-A/85
PD 11-DEC-2001
PF 28-MAR-2001 JP 2001093106
PP 10BUFUSA SERIZAWA,HIDEYUKI HARUYAMA,KAORI NAKAHARA,IKUKO PI
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AGIP19/02,AGIP29/00,AG1P37/00,AG1P37/06,AG1P37/08,AG1P43/00//
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Location/Qualifiers (humon)'.

1. 729
/organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
a _200 c _189__
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A61K37/02,C12N15/00
Drug containing humanized anti-Fas antibody
Key Location/Qualifiers
Location/Qualifiers
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Humanized anti-Fas antibody.
E40896.
E40896.1 GI:18627473
JP 2000166574-A/85.
 JP 2001342148-A/85.
Homo sapiens (human)
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PC C1
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EDFATYYCQQSYSTPRTFGQGTKVEIR"
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                                                dandhi,R., Das,J., Handa,R. and Pal,R.
Potentially disease-modifying effects of apoptotic-cell specific immune responses
immune responses
Inpublished
2 (Barbard 1988)
Pal,R.
Direct Submission
Direct Submission
Institute of Immunology, Aruna Asaf Ali Marg, JNU Complex, New Delhi, 110067, INDIA
Location/Qualifiers
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         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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/gerde="IGLV"
/product="immunoglobulin light chain variable region"
106 c 96 g 88 t
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Pred. No. 2e-100;
0; Mismatches 29;
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/gene="IGLV"
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Best Local Similarity 92.5%;
Matches 358; Conservative
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/gene="IGLV"
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Homo sapiens
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RESULT 6

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/codon_gtart=1
/product== immunoglobulin light chain"
/product== immunoglobulin light chain"
/product== immunoglobulin light
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                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
I (bases I to 390)
Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Blancher,A.and Capra,J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
2 (bases 1 to 390)
Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A. and Capra, J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
Universited 506-MAY-1996) J.S. Andris, Molecular 1000 Harry Hines
Blvd., Dallas, TX 75235-9140, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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Pred. No. 2.5e-98;
0; Mismatches 33; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Macaca mulatta"
/mol_type="mRNA"
/db_xref="taxon:9544"
/note="hybridoma 1D8"
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Best Local Similarity 91.5%;
Matches 354; Conservative
                                                                                                                                                                         US7571.1 GI:1575089
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Human monoclonal antibody against TGF-beta-II receptor and medicinal use thereof.
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121 GTCACCATCACTTGCAGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 180
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1 (bases 1 to 438)
Sakamoto,S. and Kamada,M.
Human monoclonal antibody against TGF-beta-II receptor and medicinal use thereof
Datent: JP 2001206899-A 6 31-JUL-2001;
JAPAN TOBACCO III

OS Homo Sapiens (human)
PN JP 2001206899-A/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JUL-2001
08-NOV-2000 JP 2000340216
SHINJI SAKAMOTO,MASAFUMI KAWADA
C07K16/28,A61K39/395,A61P1/16,A61P9/04,A61P9/10,A61P9/10, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A61P13/12, A61P17/00, A61P17/02, A61P17/04, A61P17/06, A61P19/02,
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C12N5/10,C12N15/02//C12P21/08
Human monoclonal antibody against TGF-beta-II receptor and
medicinal use
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                                                          181 AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
_123 c 111 g 10
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JP 2001206899-A/6.
Homo sapiens (human)
Homo sapiens
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PC A61P11
PC A61P4:
PC C12N5,
CC Human
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Best Local
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ORIGIN
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BD015544
LOCUS
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                                                                                                                                                                                E12918 197-APR-1998 Human mRNA for variable region of light chain of anti-carcinoma monoclonal antibody CLN''1-1gM, complete cds.
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1 (bases 1 to 396)
Hagiwara, H., Aozuka, Y. and Miyahara, J.
AMINO ACID SEQUENCE OF ANTICANCER HUMAN MONOCLONAL ANTIBODY AND DNA BASE SEQUENCE CODING FOR THE SAME
PATENT: JP 1997100300-A 2 15-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                댐
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214 . 234 /note='this region encodes Complementarity
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Best Local Similarity 91.5%;
Matches 354; Conservative
                                                                                                                     E12918.1 GI:3251749
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Homo sapiens (human)
Homo sapiens
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 438)

S akamoto, S. and Kamada, M.

Human monoclonal antibody for human TGF-beta type II receptor and pharmaceutical use thereoff

L JAPAN TOBACO INC, SHINUI SAKAMOTO, MASAFUMI KAMADA

OS Homo sapiens (human)

PN WO 0136642-A/6

PF 17-NOV-2000 WO 2000JP008129

PR 18-NOV-2000 WO 2000JP008129

PR 18-NOV-1999 JP 99P 328681,08-NOV-2000 JP 00P 340216 PI

SHINUI SAKAMOTO, MASAFUMI KAMADA

PC C12N15/13, CO7K16/28, C12N5/16, A61P2/09, A61P2/10, A61P2/106, A61P2/06, A61P2/100, A61P2/106, A61P2/106
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Human monoclonal antibody for human TGF-beta type II receptor and pharmaceutical use thereof.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
_123 c 111 g 101
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WO 0136642-A/6.
Homo sapiens (human)
Homo sapiens
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 406)
Aucouturier, P., Bauwens, M., Khamlichi, A.A., Denoroy, L.,
Spinelli, S., Touchard, G., Preud'homme, J.L. and Cogne, M.
Monochonal 1g L. chain vol. Chain vol. domain fragment crystallization
in myeloma-associated Fanconi's syndrome
J. Immunol. 150 (8 Pt 1), 3561-3568 (1993)
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/protein id="AAA51019.1"
/db xref="GT:189951"
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CRASOTTATPLMWYQQCRGKAPKLLYGASSLQSGVPSRFSGSGSGTDFTLTISSLQP
EDFATYYCQQSYSIPWTFGQGTKVEIKRTVAAP"
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                                                              GTCACCATCACTTGCAGGCCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG
                                                                                                                                            181 AAACCAGGAAAAGCTCCTAATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Original source text: Homo sapiens (individual_isolate patient CHEB) bone marrow CDNA to mRNA.

Location/Qualifiers
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C-region; J-region; V-region; immunoglobulin kappa-chain;
immunoglobulin 11ght chain.
Homo sapiens (human)
Homo sapiens
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/gene="IgK"
56...>406
/gene="IgK"
/product="immunoglobulin kappa chain"
56...388
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M87478
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/tissue_type="bone marrow"
/ . .406
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/mol type="mRNA"
/isoTate="patient CHEB"
/db_xref="taxon:9606"
/map="2p12"
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/codon_start=1
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2. .>406
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/gene="IgK"
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/product="imminoglobulin light chain variable region"
/protein id="AAR86916.1"
/db xref="G1:995293"
/translation="DMRVPAQLIGILILWIRGARCDIOMTGSPSSLSASVGDRVTITC
RASQSISNYLWWYQQRGKGPRLIHAASSLOSGVPSRFSGSGSGTDFTLTISSLQPE
DRATION_CQSYSTPRIFEGGGTVEIRIRAR"

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                                                                                                       /note="isolated from B-cell chronic lymphocytic leukemia
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Homo sapiens, similar to anti TNF-alpha antibody light-chain Fab
fragment, clone MGC:32713 IMAGE:4691280, mRNA, complete cds.
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Direct Submission
Submitted (02-JUJ-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
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/product="immunoglobulin light chain variable region"
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/note="unmutated"
                 /chromosome="14"
/map="14q32-q39"
/clone="BUS"
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Mammalia; Eutheria;
1 (bases 1 to 962)
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                                                //Joce="This CDS feature is included to show the translation of the corresponding C_region. Presently translation qualifiers on C_region features are illegal." /codon statt=! /protein_id="AAAS1020.1" /db_xref="GT:561655" /translation="RTVAAP" |
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Homo sapiens clone BUS immunoglobulin light chain variable region
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Maloum, K., Dighiero, G. and Magnac, C.C.
Unmutated Ig VH genes in CLL patients
Unpublished

Z. (bases I to 400)

Maloum, K., Dighiero, G. and Magnac, C.C.
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Pred. No. 8.5e-98;
0; Mismatches 34
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/mol_type="genomic DNA"
'note="V1-J1 region"
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ilarity 91.2%;
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/gene="IgK"
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                        유
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbbe.r@mail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.AG.E. Consortium (LLML)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNI at: http://image.llnl.gov Series: IRAL Plates 41 Row: j Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAATCAGCAGCCTG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26. .736
/codon_start=1
/product="similar to anti TNF-alpha antibody light-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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Pred. No. 3e-97;
n. Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="MGC:32713 IMAGE:4691280"
fissue_type="Lung"
/clone_lib="NIH MGC_77"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pDNR-LIB"
                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Best Local Similarity 91.0%;
Matches 352; Conservative
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                                                                                                                                                                                                                                                                                                                       prediction.
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HUMIGKVCA 432 bp mRNA linear PRI 05-MAY-2000
HOmo sapiens immunoglobulin kappa light chain VC region (IGK) mRNA,
partial cds.
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CRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQP
EDFATYYCQQSYSTPPWTFGQGTKVEIKRTVAAPSVFIFPPS"
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 432)

Friedman, D.F., Moore, J.S., Erikson, J., Manz, J., Goldman, J., Nowell, P.C. and Silberstein, L.E.
Variable region gene analysis of an isotype-switched (IgA) variant of enronic lymphocytic leukemia
Blood 80 (9), 2287-2297 (1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/product="immunoglobulin kappa light chain VC region"
/protein_iaAAA59089.1"
/db_xref="GI:185985"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /ceil_type="lymphoblast"
/tissue_type="chronic lymphocytic leukemia blood"
/dev_stāge="adult"
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Pred. No. 3.3e-97;
0; Mismatches 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol type="mRNA"
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/map="2p12"
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                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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/note="G00-119-341"
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Best Local Similarity 92.3%;
Matches 360; Conservative
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/gene="IGK"
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                                                                                                                                                    Homo sapiens (human)
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                                                                                                          L01279.1 GI:185984
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180

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/translation="wdmrvdaqulglililmppgsrcdiowtospssvsasvddrvtit
crasqgisrllawyqqkpgkapklliyvasslqsgvpsrfsgsgsgtdftlisslqp
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fyprbakvqowkydakliqsgvsqbsytsgdstysllskadyrbkHkvyacev
thqglsspvtkspnrgec"
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                                                                                                                                 CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
                                                                                                                                                   CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG 300
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                   GTCACCTTCACTTGCAGGGCAAGTGAGAACGTTAACAACTTTACATTGGTATCAGCAG
GTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG
                                                                                   AAACCAGGAAAAGCTCCTAATCTTATGTTGCATCCAGTTTGCAAAGTGGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takashi,T., Katsunari,T.P. and Nobuaki,H.
Muman monoclonal antibody against a costimulatory signal
transduction molecule allim and pharmaceutical use thereof
Patent: EP 1158004-A 29 28-NOV-2001;
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39. .749
/note="unnamed protein product"
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// Organism="Homo sapiens"
// mol_type="genomic DNA"
// db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 29 from Patent EP1158004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAD19026.1"
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                                                                                                                                                                                                                                                                                                         GCCGCAGGCCAAGGTGCAGATCAAA 387
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Homo sapiens
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CDS
                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
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KEYWORDS
SOURCE
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CRASENVNNYLHWYQQKPGKAPKLLIYGASTLQSGVPSRFSGSGSGTDFTLTISSLQP
EDVATYYCQHSYGTPLTFGGGTKVEIKR"
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                                                                                     61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria, Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca. [ (basea 1 to 390) Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Blancher,A.and Capra,J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 390)
Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
and Capra, J.D.
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Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
University of Texas Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 75235-9140, USA
Location/Qualifiers
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                   AAACCAGGGAAAAGCCCCTAAAGCTCCTGATCTATGCTGCTGCATCCAGTTTGCAAAGTGGGGTC
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protein id="AAB09456.1"
db_xref="GI:1575106"
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0; Mismatches 36
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/mol_type="mRNA"
/db_xref="taxon:9544"
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Search completed: December 29, 2003, 19:01:27 Job time : 1605.14 secs

Scoring table:

Searched:

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Perfect score:

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CB 1 (bases 1 to 493)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
LUpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
CONA Gistribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
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UI-HF-BLO-abp-a-02-0-UI.rl NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3057290 5', mRNA sequence.
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CB984750
CB986279
CB956923
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               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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IMAGE:30354121 5', mRNA sequence.
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
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Location/Qualifiers
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                                                                                                                                                         /tissue type="lymph"
/cell_type="germinal center B cells"
/cell_type="germinal center B cells"
/cell_type="germinal center B cells"
/cell_type="germinal center B cells"
/lab_fost="nH10B (LTI)"
/clone lib="NIH MGC_37"
/note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionaled cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michel Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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NIH-WGC http://mgc.noi.nih.gov/.
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AGENCOURT 13640497 NIH MGC_184 Homo sapiens cDNA clone IMAGE:30328622 5', mRNA sequence.
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                                                               organism="Homo sapiens'
                                                                                       /mol_type="mRNA"
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/clone="IMAGE:3057290"
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Homo sapiens
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/organism="Homo sapiens"
// mol_type="mRNA"
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// db_tref="Laxon:9606"
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                                                                                            BUSHIRS linear EST 16-AUG-2002
AGENCOURT_8616470 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6302159
5', mRNA sequence.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapDs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can http://image.llnl.gov
http://image.llnl.gov
c column: 24
High quality sequence stop: 672.
Location/Qualifiers
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Pred. No. 6.4e-91;
0; Mismatches 29;
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Mammalia; Eutheria; Primates;
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/lab host="DH10B (T1 phage-resistant)"
/lab host="DH10B (T1 phage-resistant)"
/clone="Drgan: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
Sfi1 (ggccattatggcc); Site_2: Sfi1 (ggccgcctggcc);
Library is oligo-dT primed and directionally cloned.
Colored from a glandular pool of tissues from thyoid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb): 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
                                                                                                                                                                                                                                                                                                                                  Email: crapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (Linl.)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCMISS row: p column: 02
High quality sequence stop: 549.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases: 1 to 72,4)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGCTCCTTCTGGCTCCCAGGTGCC
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michel Brownstein and Dr. Miklos Palkovits
Tissue Procurement: Dr. Michel Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCMI33 row: k column: 22
High quality sequence stop: 412.
High quality sequence stop: 412.
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NIH-MGC http://mgc.nci.nih.gov/.
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Pred. No. 1.8e-90;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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1 (Dases 1 to 969)
NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
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Tissue produrement: Dr. Mark Watson
Tissue produrement: Dr. Mark Watson
CDNA Library Pepsaration: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can bfound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llh.gov
Plate: LLCM2470 row: h column: 03
High quality sequence stop: 640.
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ss, Inc.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can k
Glound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
n column: 20
High quality sequence stop: 408.
High quality sequence stop: 408.
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CB956923 708 bp mRNA linear EST 29-APR-2003 AGENCOURT 13778921 NIH MGC 184 Homo sapiens cDNA clone IMAGE:30351494 5', mRNA sequence.
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Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
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/lab host="INAGE:30351494"
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NIH MGC 184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
Sfil (ggccattatgggc); Site_2: Sfil (ggccgctcggcc);
Library is oligo-dT primed and directionally cloned. cDNA
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1 (bases 1 to 708)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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   Length
                                                               Indels
DB 14;
   Score 337.4; DB 1.
Pred. No. 5.3e-90;
0; Mismatches 31
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Location/Qualifiers
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/db_xref="taxon:9606"
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CB985168
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                                                                                                                                                                                      DB 14; Length 708;
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AGENCOURT 13784991 NIH MGC 184 Homo sapiens cDNA clone
IMAGE:30352433 5′, mRNA sequence.
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                                                                                                                                                                                      86.8%; Score 335.8; DB 1. 91.7%; Pred. No. 1.5e-89; ive 0; Mismatches 32
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                                                                                                                                                                                                                 355; Conservative
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AGENCOURT 13438717 NIH MGC 184 Homo mapiens cDNA clone
IMAGE:30326564 S', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 763)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Pred. No. 1.6e-89;
0; Mismatches 32;
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organism="Homo sapiens"
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ilarity 91.7%;
Conservative 0
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nes 355; Conserv
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COMMENT

FEATURES

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/organism= mRNAm
/db_xref="taxon:9606"
/clone="INAGE:30328513"
/lab_host="DH108 (T1 phage-resistant)"
/lab_host="DH108 (T1 phage-resistant)"
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Sfi1 (ggccattarggcc); Site_2: Sfi1 (ggccattarggcc);
Library is oligo-dT primed and directionally cloned.
Darathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR: This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Produrement: Dr. Michael Brownstein and Dr. Miklos Palkovits
Tissue Produrement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llhl.gov
Plate: NDCM19 row: e column: 02
High quality sequence stops: 555.
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                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 750)
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NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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207 c 190 g 153 t 5 ot
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llarity 91.2%; Pred. No. 1.4e-88;
Conservative 0; Mismatches 34
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                             GI:30279919
                                                                                    Homo sapiens
                                                                                                                 sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /done="IMAGE:3036564"
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NHHMGC:181664"
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NHHMGC:18166-Glandular; Vector: pDNR-LIB; Site_1:
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
Sfil (ggccattatggcc); Site_2: Sfil (ggccgcctcggcc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyoid,
parathyroid, adrenal, cortex and pineal gland. S' and 3'
adaptors were used in cloning as follows: S' adaptor
sequence: S'-CACGCGATTATGGCC-3' and 3' adaptor sequence:
S'-ATTCTAGAGGCCGATATGGCC-3' and 3' adaptor sequence:
S'-ATTCTAGAGGCCGACATTG-dT(30)BN-3' (Where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3: Skb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clonech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."
                 Email: cgapbs-remail.min.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM34 row: c column: 21
High quality sequence stop: 602.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 GTCACCATCACTTGCCGGCCAAGTCACGACATTAGAAGTGATTTAGGCTGGTATCAGCAG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 AAAGCAGGGAAAGCCCCTAAGTTCCTGATCTATGGTGCATCCAATTTACAGAGTGGGGTC 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCATCAAGGTTCAGCGCCAGTGCATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
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Pred. No. 4.8e-89;
0; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                    1. .763
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch 86.4%; al Similarity 91.5%; 354; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
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CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
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Best Local Similarity 91.2%;
Matches 352; Conservative 0
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                                                                                                                                                                                                                                                                                                       sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG540787 891 bp mRNA linear EST 03-APR-2001
602570674F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4695114 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GICACCATCACTTGCAGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 AGATGTGACATCCAGTTGACCCAGTCTCCATCCTTCCTGTCTGCATCTGTAGGAGACAGA 145
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                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 891)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                     Email: cgapbe-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMISSO row: c column: 19
High quality Sequence stop: 577.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 85.9%; Score 332.6; DB 10; Length 891; al Similarity 91.2%; Pred. No. 1.6e-88; 353; Conservative 0; Mismatches 34; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34; Indels
 'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
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                                                                                                                                       BG540787.1 GI:13533020
                                                                                                                                                                                Homo sapiens (human)
                                                                                                                             mRNA sequence.
                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                              Unpublished
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                                                                                     BG540787
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/organism="Homo sapiens"
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dlone="CSOD1026YL22"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/clone_Tist strand cDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and BCOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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25-NORMALIZED Homo sapiens CDNA
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                                                                                                                                           67 regacareaegerecececreaerecreseserecrecrecrecresereceaegreea 126
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                                                                                                301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC 360
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Li, W. B., Gruber, C., Jessee, J., and Polayes, D.
Full-length, CDNA libraries and normalization
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
more information about this cluster, see
http://www.genoscope.cns.fr/
http://www.genoscope.cns.fr/
Feng Liang Email : fliangelifetech.com URL:
http://fulllangth.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO26DF11QP1.
266 CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAATCAGCAGGCCTG
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Pred. No. 3.2e-88;
0; Mismatches 34; Indels
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120

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DEFINITION

CB957909

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS TITLE JOURNAL COMMENT

REFERENCE

242 307

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/MOI type="mRNA"
// Ab Arref="mRNA"
// Ab Arref="mRNA"
// Ab Arref="mRNA"
// Ab host="mAnd"
// Ab host
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Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://mage.llnl.gov
Plate: NDCM154 row: i column: 13
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 764)
29 ATGGACATGAGGGTCCCCGCTCAGGGCTCCTTCTACTCTGGCTCCCGAGGTGCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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/organism="Homo sapiens"
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Location/Qualifiers
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TITLE
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M. A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M. A.G.E. Consortium/LLNL at:
http://image.llnl.gov
e column: 12
High quality sequence stop: 407.
Location/Qualifiers
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(roganism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="INAGE:30349643"

/clone="TMAGE:30349643"

/clone="TMH MGC 184"

/clone lib="NHH MGC 184"

/clone lib="NHH MGC 184"

/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
                                                          247 AACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGGTCC 306
                                                                                                                                                                                                                       CATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGC 366
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 743)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
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Matches 352, Conservative
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source

FEATURES

Query Match Best Local (

BASE COUNT

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                                                                                                                                                                                                                      by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH MGC Library."

214 c 203 g 151 t 4 others
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Search completed: December 29, 2003, 21:44:14 Job time : 1677.6 secs

Partial nucleotide Human IGFAM-10 imm Human IGFAM-9 immu Human anti-HBs lig

Nucleotide sequenc Anti-CD40 monoclon Anti-CD40 monoclon

DNA encoding the

Nucleotide sequenc Human immunoglobul Functional Kappa t

Human IGFAM-1 immu Anti-CD40 monoclon Anti-CD40 monoclon

Human colon cancer Anti-CD40 monoclon

Human breast cance Nucleotide sequenc Human ovarian anti Human colon tumour Functional kappa t Human immunoglobul Nucleotide sequenc Partial nucleotide

Human pancreatic t 93KA9 anti-Varicel

Human anti-RSV mon Humanized 1308F VL Hu1308 VL encoding Human IGFAM-13 imm Human dithp antige

Nucleotide sequenc Human immunoglobul Synthetic kappa li Nucleotide sequenc Human colon tumour Kappa light chain

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Database

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Anti-human CD23 5E8 monoclonal antibody light chain variable region DNA
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/product= "anti-human CD23 5E8 light chain variable
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/note= "encodes CDR 1 region"
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AAZ31870
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(c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Best Local Similarity 100.0%; Pred. No. 1.6e-108;
Matches 387; Conservative 0; Mismatches 0; Indels 0;
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/note= "encodes CDR 2 region"
331..357
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/note= "encodes CDR 3 region"
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Chimeric - Baculovirus.
Chimeric - Cytomegalovirus.
Chimeric - Cytomegalovirus.
Chimeric - Rhesus macaque polyoma virus.
Location/Qualifiers
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This is the nucleotide sequence of novel target plasmid Mandy. The plasmid includes an inactivated murine dihydrofolate reductase (DHFR) gene, the Escherichia coli beta-galactosidase gene, baculovirus DNA, a cassette comprising the promoter and enhancer elements from cytomegalovirus and SV40 virus, the E. coli clements from cytomegalovirus and SV40 virus, the E. coli clements from cytomegalovirus and SV40 virus, the E. coli clements from cytomegalovirus and SV40 virus, the E. coli clements from cytomegalovirus and SV40 virus, the E. coli clear and transposon Th5 heomycin phosphotransferase gene, an inactivated Salmonella typhimurium histidinol dehydrogenase (HisD) gene and transposon Th5 heomycin phosphotransferase (neo) gene and transposon Th5 neomycin phosphotransferase (neo) gene invention provides a novel method for integrating a desired invention provides a novel method for integrating a desired coll vita homologous recombination. This involves transfecting the cell vita handlogous recombination with the unique sequence which provides for homologous recombination with the unique sequence which provides for homologous recombination with the unique sequence which provides for monologous recombination with the unique sequence contains in the marker plasmid, and further comprising a desired DNA that is to be integrated into the mammalian cells, typically an the monologous recombination system utilises the neo gene as a dominant selectable marker. The neo gene is split into 3 sexons. Exon 3 is present on the marker plasmid and becomes integrated into the mammalian cells. Exon 3 is present on the marker plasmid and are separated by an intron into which at the targeting plasmid, and are separated by an intron into which at the targeting plasmid, and are separated by an intron into which at the targeting vertor with the integrated into vertor with the integrated by an intron into well the tenulation of integrated into vertor with the integrated by an intron into well the tenulation of integrated into vertor with t mammalian cells, and can be used to express any type of recombinant protein. The use of a triply spliced selectable marker means that all selected colonies arise from homologous recombination. In of the targeting vector with the integrated marking vector results in correct splicing of all 3 exons of the neo gene and expression of a functional neo protein. The method is applicable to all can e.9 addition, the number of colonies that need to be screened to identify high producer clones is reduced. An amplifiable gene be inserted on integration of the marking vector, so that when qene is targeted to this site, the gene is further enhanced by comprises homologous recombination using specific integration of DNA in mammals for selectable marker and target plasmids Example 1; Fig 10; 114pp; English lobuling amplification [mmnnod] Site 

Sequence 19035 BP; 4705 A; 4968 C; 4822 G; 4519 T; 21 other;

Length 19035;

7600 ö 120 09 7541 Arggacargaggrecegerchaerecraggerecricitergereregereceaggreee AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA Gaps ô 1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGG Indels Score 387; DB 19; Pred. No. 7.1e-108; .. 0 0; Mismatches 100.0%; 387; Conservative Query Match Best Local Similarity 61 Best Loca Matches ઠે ð

7661 GTCACCATCACTTGCAGGCAAGTCAGGACATTAGGTATTAAATTGGTATCAGCAG 7720 180 GTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 121 · 8 셤

7601 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 7660

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7721 AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC 7780

181 AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC

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240

241 CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300

DB 21; Length 729;

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multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (1) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (1) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a human immunoglobulin light chain kappa variable region subgroup type I which is used in the construction of humanised anti-Fas antibody
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               CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 7840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiatreriosolacotic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosolerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.
                                                                                                                                 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunoglobulin light chain kappa region subgroup type I DNA
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                                                                                                                                                                                                                                                                                                                                  GCCAAGGGACCAAGGTGGAAATCAAA 7927
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98JP-0276882.
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                             Gaps
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light chain subunit; apoptosis; immunosuppressive; antiallergic;
autoimmune disease; allergy; atopic; PCR primer; ss.
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                                                          1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGC
                            28; Indela
Score 342.2; DB 2
Pred. No. 1.1e-94;
0; Mismatches 28
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  Query Match
Best Local Similarity 92.8%;
Matches 359; Conservative
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The invention relates to a preventive or treating agent for diseases caused by abnormality in Fas/Fas ligand system containing as the active component an antibody having as the light chain subunit a polypeptide containing residues 1-218 of one of 3, 239 residue amino acid sequences, or residues 1-451 of one of 3, 470 residue amino acid sequences, fully defined in the specification and having an activity of combining specifically with mammalian Fas and an activity of inducing apoptosis in a cell expressing Fas. The agent has immunosuppressive and antiallergic activity and is used for preventing and treating autoimmune diseases, allergy, atopy and others. The present sequence is that of a PCR primer, useful to the invention.
                                                                    anti-Fas antibody, used for preventing and
                                                                                                                                         Example 15 (Preparatory); Page 40; 194pp; Japanese.
                                                                                           treating autoimmune diseases, allergy, and atopy
                                                                  containing humanised
                    WPI; 2002-145113/19
                                                                  Drug
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Seguence 729 BP; 192 A; 200 C; 182 G; 155 T; 0 other;

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88.4%; Score 342.2; DB 24; Length 729;
                                      0; Mismatches 28; Indels
                  Pred. No. 1.1e-94;
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                  92.8%;
                                    Matches 359; Conservative
                    Best Local Similarity
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ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyclt, dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; rinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; Human ovarian antigen HRACW30 cDNA, SEQ ID NO:121. ВР ABQ54241 standard; cDNA; 1106 (first entry) 22-AUG-2002 AB054241; RESULT 5 ABQ54241
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Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; chromosome 2p12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
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Claim 1; SEQ ID No 121; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABO\$4131-ABQ\$6305), and also encompasses polypeptides the inventical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens to compare the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens of compare the sequences of the invention. The invention and the use convertion antigen polynucleotides and polyneptides in diagnosing, treating, prognosing or preventing various ovary and/or breast related disorders. Such conditions include ovarian cancer and breast cancer, and disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune cophoritis, systemic lupus erythematosus, blood-related disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and conditions conditions or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the modulate ovarian antigen expression or activity. The polynucleotides may disease diagnosis, drug targeting and phenotyping. The present effections conditions or to prepare antibodies engely energing and phenotyping. The present effections conditions and page to the present effections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Gaps ; 0 Score 339; DB 24; Length 1106; Pred. No. 1.2e-93; 7; Mismatches 29; Indels 0 Sequence 1106 BP; 321 A; 296 C; 247 G; 227 T; 15 other; 87.6**%**; 90.7**%**; Matches' 351; Conservative Local Similarity

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                                         AAACCAGGAAAAGCTCCTAAGCTCCTGATCTAGCTTCCAGTTTGCAAAGTGGGGGTC
                                                                                                                             CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC
                                                                                                                                                                                                                                                                                                                Human anti-tumour antigen antibody light chain variable region cDNA
                                                                                                                                                                                                                                                                                                                                  Human; tumour antigen; cancer; monoclonal; antibody; light chain; variable region; medicine; pharmacology; biochemistry; ds.
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86.4%; Score 334.2; DB 18; Length 396;
Best Local Similarity 91.5%; Pred. No. 2.4e-92;
Matches 354; Conservative 0; Mismatches 33; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a human anti-tumour antigen monoclonal antibody (MAb) light chain variable region, useful medicine, pharmacology and biochemietry. The isotype of a MAD secreted by the human/human hybridoma HT was determined to be and kappa. Human MAb was purified, and the antigen recognised human MAb CLN"-IGM identified by western blotting.
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                                                                                                                                                                                  Socation/Qualifiers
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The present invention relates to novel human monoclonal antibodies. The antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II receptor, resulting in the inhibition of the signal transduction of human TGF-beta into cells. The antibodies can be used for the prevention and treatment of diseases associated with the production of TGF-beta, such as tissue fibrosis in the lung, liver, skin, kidney or other tissues,
                                                                                                                                                                              240
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                                                                                                                                                                                                                                            241 CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
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                                                                                                                                 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC 360
                                                                                                                                                                                                                                                                                                                             GTCACCATCACTTGCAGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, antiarthritic, cardiant, monoclonal antibody, keloid, arthritis, Tumour Growth Factor-beta II receptor, TGF-beta II receptor; atopy, signal transduction inhibition, tissue fibrosis, atherosclerosis, ds.
                                                              61 AGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGAGAGACAGA
                                                                                                                                                                              AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 12; Page 103-104; 118pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                              GGCCAAGGGACCAAGGTGGAAATCAAA 387
                                                                                                                                                                                                                                                                                                                                                                                               Human coding sequence SEQ ID 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH41157 standard; DNA; 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NISB ) JAPAN TOBACCO
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AAA46899 standard; DNA; 714
              WPI; 2002-075313/10.
P-PSDB; AAU74297.
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                                                                                                                                                                                    AGGTGTGACATCCAGATGACCCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGA 120
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atherosclerosis, atopy, keloid and arthritis. The present sequence was used in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus; multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis; allergic contact-type dermatitis; chronic inflammatory dermatosis; systemic lupus erythematosus; autoimmune disorder; inflammation; ss;
                                                                                                                                                                                                                                                                                                            CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCTG
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                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              graft versus host reaction; immune rejection; intestinal immunity; ulcerative colitis; pancreatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiallergic, antiuleer, neuroprotective, antithyroid, vasotropic, immunosuppressive, dermatological, antiinflammatory, hepatotropic, activation inducible lymphocyte immunomodulatory molecule, AILIM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
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                                                              Length 438;
                                                           Score 334.2; DB 22; Length
Pred. No. 2.5e-92;
0; Mismatches 33; Indels
                                      Sequence 438 BP; 103 A; 123 C; 111 G; 101 T; 0 other;
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                                                             Query Match
Best Local Similarity 91.5%;
Matches 354; Conservative
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30-MAR-2001; 2001JP-0099508.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAR-2002
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                                                                                                                                                                                                                                      The invention relates to a novel human antibody (I), preferably a human monoclonal antibody which binds to an activation inducible lymphocyte immunomodulatory molecule (AILIM). (I) is useful for modulating signal transduction into a cell mediated by ALLIM, for modulating proliferation of ALLIM-expressing cells, for modulating production of a cytokine from AILIM-expressing cells, and for inducing antibody-dependent cytotoxicity against AILIM-expressing cells and/or immune cytolysis or apoptosis of AILIM-expressing cells (I) is useful for treating or apoptosis of prophylaxis of delayed type allergy. (I) is useful for treating and preventing various diseases associated with AILIM-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preventing various treases associated with Annia decorporation of the diseases. (1) is useful for suppression, advancement of the diseases. (1) is useful for suppression, prevention and/or treatment of rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis, allergic context-type dermatitis, chronic inflammatory dermatosis, systemic lupus erythematosus, insulin-dependent diabetes mellitus, psoriasis, autoimmune or allergic disorders, inflammation, graft versus host reaction, graft versus host disease, immune rejection, disorders caused by abnormal intestinal ulcerative colitis, pneumonia, hepatitis, nephritis, vasculitis, and pancreatitis. (1) induces no serious immunorejection due to antigenicity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human anti-mouse antigenicity (HAMA) in a host. 7 represent anti-human AILIM monoclonal antibody coding
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New human monoclonal antibody that binds to activation inducible lymphocyte immunomodulatory molecule, useful for treating rheumatoid arthritis, multiple sclerosis and inflammation
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0; Mismatches
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                                                                                                                                                                  Claim 45; Page 267-270; 300pp; English.
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Matches 351; Conservative
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AAS99444-AAS99477
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CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
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P-PSDB; AAY56659, AAY56724.
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Matches 348, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGATGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTTAAATTGGTATCAGCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCACCATCACTTGCCGGGCAAGTCAGAGCATTAACAGCTATTTAGATTGGTATTCAGCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                 Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system; hyperimmunity disorder; autoimmune disease; diabetes; graft rejection; proliferative disorder; cancer; immunodeficient disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Aregacareaecercecreaecrecreaecrecrecrecracrecreserces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)-4 containing specified heavy and light chain sequences, useful for treating, e.g. immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes a kappa chain of an antibody of the invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)-4. Antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a FRI-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in CDR1, CDR2 and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity disorders (e.g. autoimmune disease, diabetes and graft rejection) and proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate immune system to up-regulate immunodeficient disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Davis CG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21; Length 714;
                                                                   the kappa chain of immunoglobulin clone 11.2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gilman SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence 714 BP; 188 A; 199 C; 173 G; 154 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 326.2; DB 2.
Pred. No. 8.6e-90;
0; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanke JH,
                                                                                                                                                                                                      Location/Qualifiers
67..714
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mueller EE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Fig 22r; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.3%;
90.2%;
                                                                                                                                                                                                                                                                                                                                         99WO-US30895
                                                                                                                                                                                                                                                                                                                                                                        98US-0113647
                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neveu MJ,
                                                                                                                                                                                                                                                                                                                                                                                                        (PFIZ ) PFIZER INC. (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-442647/38.
P-PSDB; AAY93735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                         WO200037504-A2
                                                                     DNA encoding
                                                                                                                                                                                                                                                                                                                                         23-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                          23-DEC-1998;
                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corvalan JR;
                                  03-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Simi
Matches 349;
                                                                                                                                                                                                                                                                                                        29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanson DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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     AAA46899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibodies containing donor complementarity determining regions and non-human primate acceptor frameworks, having reduced immunogenicity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complementarity determining region; antibody; primate; immunogenicity; Old World ape; Old World monkey; antigen-binding affinity; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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89.9%; Pred. No. 2.1e-89;
iive 0; Mismatches 39; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of chimpanzee Vkappa cDNA clone 46-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 387 BP; 94 A; 104 C; 95 G; 94 T; 0 other;
                                                                                                                                                                                                                                           GGCCAAGGGACCAAGGTGGAAATCAAA 387
                                                                                                                                                                                                                                                                                       Example 2; Page 67-68; 123pp; English.
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Gaps

3; 448;

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for autoimmune diseases, allergy or coagulation factor VIII inhibitors syndrome. This polynucleotide sequence represents a coding DNA sequence relating to the anti-CD40 monoclonal antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antiallergic; haemostatic; immunomodulator; cytostatic; antibody; human CD40; IL-12; LPS; lipopolysaccharide; IFNgamma; interferon gamma; dendritic cell; high G28-5; CD95 expression; high G28-5; B cell line;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoactivator, anti-tumour agent, immunosuppressant, allergy, autoimmune disease, coagulation factor VIII inhibitor, anti-CD40; gene,
                                                                                                                                                                                                                             61 AGATGTGACATCCAGATGACCCAGTCTCCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA
                                                                                                                                                                                                                                                                                                         GTCACCATCACTTGCAGGCCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                          <u> AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATTTGCAAAGTGGGGGTC</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAACCAGGGAAAGCTCCTAAAGCTCCTGATCTATGATGCCTCCAATTTGGAAAGTGGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ccarcaaggricagcggcagrggarcrggacagarrrcacrcrcaccarcagcagccrg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              caeccidaadaririrgcaacrirarracrercaacagriraaragriracce---Gacerre
                                                                                                                                                                                                      ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGCC
                                                                                                                       DB 25; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ż
                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-CD40 monoclonal antibody related DNA SEQ ID No 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takahashi
                                                                                Sequence 448 BP; 111 A; 123 C; 114 G; 100 T; 0 other;
                                                                                                                                                               29;
                                                                                                                                            .2e-89;
                                                                                                                   Score 324.6; D
Pred. No. 2.2e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCCAAGGGACCAAGGTGGAAATCAAA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCCAAGGGACCAAGGTGGAAATCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Force WR,
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2001JP-0142482.
2001JP-0310535.
2001US-0040244.
                                                                                                                     Query Match 83.9%;
Best Local Similarity 91.7%;
Matches 355; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ř
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABT31882 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KIRI ) KIRIN BEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200288186-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-APR-2001;
11-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mikayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fragment, has at least one of the following properties: acting on dendritic cells to produce IL-12 in the presence of LPS (lipopolysaccharide) and IFNGamma (interferon gamma); acting on dendritic cells to activate maturity of the dendritic cells with high G28-5 antibody, and activating CD95 expression with high G28-5 antibody against B cell line. Such antibodies or functional fragments can be used as immunoactivators, anti-tumour agents, immunosuppressants, and as remedies
                                                                                                       240
                                                                                                                                            240
                                                                                                                                                                                     300
                                                                                                                                                                                                                                                                                         CAACCTGAAGATTTTGCAACTTATTACTGTCAGGTGGTTACGGTACGCTTTC 360
                          GTCACCATCACTTGCAGGCCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 180
                                                           Greacearcactreceggeaagreaggearrageaactarragagrregrareageae 180
                                                                                                                                                                                                                           ccarcaagerrcagregeagregarcregaacagarrrcacrercaccarcagagrerg 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antiallergic; haemostatic; immunomodulator; cytostatic; antibody; human CD40; IL-12; LPS; lipopolysaccharide; IFNgamma; interferon gamma; dendritic cell; high G28-5; CSPS expression; high G28-5; B cell line; immunoactivator; anti-tumour agent; immunosuppressant; allergy; autoimmune disease; coagulation factor VIII inhibitor; anti-CD40; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to CD40,
                                                                                                                                                                                   CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCGGCCTG
                                                                                                                                                                                                                                                                    CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC
                                                                                                                                            AAACCAGGGAAAGCCCCTAAGCTCCTGATCTATTATGCATCCACTTTGCAAAGTGGGGTC
                                                                                                         <u>AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD40 or functional fragment, is useful in the treatment of e.g. autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an antibody to human CD40, or its functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-CD40 monoclonal antibody related DNA SEQ ID No 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen X,
                                                                                                                                                                                                                                                                                                                                                387
                                                                                                                                                                                                                                                                                                                                                                                        GGTGGAGGACCAAGGTGGAGATCAAA 387
                                                                                                                                                                                                                                                                                                                                              GGCCAAGGGACCAAGGTGGAAATCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 26; Page 52-53; 94pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Force
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2001JP-0142482.
2001JP-0310535.
2001US-0040244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABT31874 standard; DNA; 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-APR-2002; 2002WO-JP04292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KIRI ) KIRIN BEER KK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diseases or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-120463/
P-PSDB; ABJ36932.
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11-MAY-2001; 2
05-OCT-2001; 2
26-OCT-2001; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mikayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2003
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ABT31874;

RESULT 11 ABT31874

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CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AGATGTGACATCCAGATGACCCAGTCTCCTTCTTCTTGTCTGCATCTGTAGGAGACAGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCACCATCACTTGCAGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 Grcaccarcacradecadecadrendes artracaacres radecades 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides an antibody (Ab) comprising donor CDRs (complementarity determining regions) derived from a non-human antigenspecific donor antibody, and an acceptor framework from a non-human primate. The Abs are prepared by grafting CDRs from a non-human antigenspecific donor antibody onto homologous Old World ape or monkey acceptor frameworks. The Abs have reduced immunogenicity and are better tolerated in humans (because of the close similarity between the human and primate proteins), but retain the full antigen-binding affinity of the donor
                                                                                                                                                                                                                                                                                                                          Antibodies containing donor complementarity determining regions and non-human primate acceptor frameworks, having reduced immunogenicity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Arecacardadestrococcocroadorocreses en arecacardorocroadereco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 390 BP; 91 A; 111 C; 96 G; 92 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 83.0%; Score 321.4; DB Local Similarity 89.4%; Pred. No. 2e-88; ees 346; Conservative 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCCAAGGGACCAAGGTGGAAATCAAA 387
                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Page 96-97; 123pp; English
                                                                                                                                                  SMIK ) SMITHKLINE BEECHAM CORP.
                                                 99WO-US09131.
                                                                                                98US-0083367.
                                                                                                                                                                                                                                                   WPI; 2000-023265/02.
P-PSDB; AAY56672, AAY56737.
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                                                 28-APR-1999;
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04-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                fragment, has at least one of the following properties: acting on dendritic cells to produce IL-12 in the presence of LPS (lipopolysaccharide) and IPNgamma (interferon gamma); acting on dendritic cells to activate macurity of the dendritic cells with high G28-5 antibody; and activating CD95 expression with high G28-5 antibody against be cell line. Such antibodies or functional fragments can be used as immunoactivators, anti-tumour agents, immunosuppressants, and as remedies for autoimmune diseases, allergy or coagulation factor VIII inhibitors syndrome. This polynuclectide sequence represents a coding DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGATGCGACATCCAGATGACCCCAGTCTCCATCTTCCGTGTCTGGATCTGTAGGAGACAGA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCACCATCACTTGTCGGGCGAGTCAGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCCATCCAGATTGCCAAAGTGGGGTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ccarcaaggricagcggcagriggarringgacagarricacrcrcaccarcagcagccrg 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAGCAGTTTCCCTCGGACATTC 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGGATCCAGTTTGCAAAGTGGGGTC 298
                                                                           CD40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunogenicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCGTTCCCAGGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGGACATGAGGGTCCCCCCTCAGCTCCTGGGCTCTCTGCTCTGGCTCCCAGGTGCC
                                                                           oclonal antibody with antagonist/agonist activity to CD40 fragment, is useful in the treatment of e.g. autoimmune
                                                                                                                                                                                                                              The invention relates to an antibody to human CD40, or its functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       relating to the anti-CD40 monoclonal antibody of the invention
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Old World ape; Old World monkey; antigen-binding affinity; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
83.5%; Score 323; DB 25; Length 728;
Best Local Similarity 89.7%; Pred. No. 8.3e-89;
Matches 347; Conservative 0; Mismatches 40; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 728 BP; 183 A; 201 C; 195 G; 149 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCCAAGGGACCAAGGTGGAGATCAAA 445
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                                                                                                                                                                               Claim 16; Page 59-60; 94pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ39340 standard; DNA; 390
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                                                                           Anti-CD40 monoclonal
  WPI; 2003-120463/11
P-PSDB; ABJ36940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca cynomolgus
                                                                                                        functional
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Length 390; Indels

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Human immunoglobulin light chain variable region partial transcript.

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A novel composition has been developed which comprises an immunoglobulin (IG) having an affinity constant (Ka) of at least 2 multiply 1000000000 M-1 for binding to a predetermined human antigen. The present sequence represents a human light chain variable region partial nuclectide sequence, 10CS kappa, which encodes an amino acid sequence from a claimed immunoglobulin that specifically binds human CD4. The anti-CD4 antibodies may be used in therapeutic and diagnostic applications, especially for the treatment of human diseases. These autoimmune reactions, inflammatory response and transplant rejection. Transgenic animals are capable of producing heterologous antibodies of funding isotypes by undergoing isotype switching. These animals produce a first IG type that is necessary for antigen-stimulated B-cell maturation and can switch to encode and produce one or more subsequent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGATGCGACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
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             Ig, affinity constant; human; antigen; hybridoma; B cell; transgene; transgenic; mouse; CD4; antibody; autoimmune; inflammatory; transplant rejection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.2%; Score 318.2; DB 18; Length 388; 88.9%; Pred, No. 1.9e-87; ive 0; Mismatches 43; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                             Novel anti-CD4 antibody produced by transgenic mice - used treatment of auto-immune disease etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 44; Page 255; 396pp; English.
                                                                                                                                                                                                                                   95US-0544404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 344; Conservative
                                                                                                                                                                                                                                                                     (GENP-) GENPHARM INT INC
                                                                                                                                                                                                                                                                                                                                           WPI; 1997-235888/21
                                                                                                                                                                                                                                                                                                         Lonberg N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                               10-OCT-1996;
                                                                                                                                                                                                                                   10-OCT-1995;
                                                                                        Homo sapiens
                                                                                                                          WO9713852-A1
                                                                                                                                                              17-APR-1997.
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AAV39212-41 represent functional transcripts of a human IgGKappa anti-CD4 antibody. The sequences are isolated from 5 different transgenic mouses hybridoma cell lines. The specification describes transgenic mones hybridoma cell lines. The specification describes transgenic mone human animals, especially a mouse, which are capable of producing a human heterologous antibodies of multiple isotypes by undergoing isotype switching. The transgenes are capable of functionally rearranging a heterologous diversity (D) gene in a variable-diversity-junction (V-D-U) recombination. The transgenes include a heavy chain transgene comprising at least one V, D and J gene segment, and one constant region gene segment. The immunoglobulin (Ig) light chain can segment. The gene segment and one constant region gene segment for an unit of a natioody can be used to treat reperfusion injury. CD4 binding antibodies are used to reduce undesirable autoimmune reactions, inflammatory responses and rejection of transplanted organs. The antibodies can reduce tissue damage and prolong survival in animal models of acute adult respiratory distress syndrome (ARDS) and cid induced lung injury. The antibodies can also be used for the treatment of vasculitis, septic shock, allergic reactions (e.g.
                                                                                                                                                                                                                                                                                   CD4 binding;
                                                                                                                                                                                                                                                           Transgenic animal; human heterologous antibody; transgene; isotype switching; neutrophil efflux; reperfusion injury; CD4 bindim; autofimnue reaction; inflammatory response; transplant rejection; acid induced lung injury; acute adult respiratory distress syndrome; ARDS; vasculitis; septic shock; allergic reaction; asthma;
                                                                                                                                                                                                                            Functional Kappa transcript isolated from transgenic cell line 10C5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.2%; Score 318.2; DB 19; Length 388; 88.9%; Pred. No. 1.9e-87; ive 0; Mismatches 43; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hybridoma producing antibody specific for interleukin-8 -
prevent efflux of neutrophils from vasculature, and treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 other;
                   361 GGCCAGGGGACCAAGCTGGAGATCAAA 387
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                                                                                                                AAV39239 standard; DNA; 388
                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                              cystic fibrosis; ss
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                                                                            RESULT 15
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Gaps

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Best Local Similarity 88.9 Matches 344; Conservative

361 GGCCAAGGGACCAAGGTGGAAATCAAA 387

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361 GGCCAAGGGACCAAGGTGGAAATCAAA 387
                                                   361 GGCCAGGGGACCAAGCTGAGATCAAA 387
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Search completed: December 29, 2003, 16:25:38
Job time : 169.851 secs

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JS-09-019-441-3
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2371.523 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/USO7_NEW PUB.seq:*
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18: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2244575 segs, 1713117285 residues
                                                                                                                                                                                               December 29, 2003, 19:01:43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                             OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTITY NUC Gapoxt 1.0
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Sequence 125, Applisequence 125, Applisequence 125, Applisequence 29, Applisequence 27, Applisequence 15, Applisequence 15, Applisequence 15, Applisequence 186, Applisequence 113, Applisequence 114, Appl Sequence 3, Appl: Description US-10-066-543-2025 US-10-066-543-186 US-10-066-543-18 US-10-040-244-13 US-09-844-684-11 1 US-09-019-441-3 1 US-10-103-686-3 3 US-10-316-484-125 5 US-10-216-484-125 5 US-10-153-382-18 US-09-965-63-29 US-09-965-63-29 US-09-965-63-29 US-09-965-63-27 US-09-96-648-15 US-10-040-244-15 Query Match Length DB 342.2 342.2 329.2 326.2 324.6 323 Score Result e S

		N	Sequence 56, Appl	Sequence 1210, Ap	1210,	123	Sequence 7, Appli	25,	Sequence 10, Appl	9		Sequence 26, Appl	-	Sequence 1811, Ap	Sequence 1811, Ap	378		836	9.	22,	Sequence 5, Appli	Sequence 53, Appl	81,	24,	Sequence 2039, Ap		203	Sequence 79, Appl	Sequence 19, Appl
US-10-040-244-11	US-10-158-646-55	US-09-905-243-20	US-10-158-646-56	US-09-878-178-1210	US-10-046-935-1210	US-10-146-502-1210	US-09-919-344-7	US-09-905-243-25	US-10-389-221-10	US-09-740-002-16	US-10-401-344-3	US-09-905-243-26	US-09-878-178-1811	US-10-046-935-1811	US-10-146-502-1811	US-09-918-995-37859	US-10-158-646-65	US-10-198-846-8365	US-09-905-243-56	US-09-905-243-22	US-10-221-945-5	US-09-905-243-53	US-09-800-729-81	US-09-905-243-24	US-09-878-178-2039	203	US-10-146-502-2039	US-09-800-729-79	US-09-905-243-19
15	15	σ	15	10	14	15	10	σ	13	0	13	0	10	14	15	11	15	15	6	6	15	σ	6	6	10	14	15	σ	0
698	634	384	402	520	520	520	737	387	384	705	708	372	494	494	494	490	819	583	384	372	928	390	941	387	463	463	463	066	381
9.08	80.1	80.1	80.1	79.8	79.8	79.8	79.7	79.1	79.0	78.6	78.5	78.1	78.0	78.0	78.0	77.3	77.3	77.2	77.0	76.2	75.8	75.6	74.5	74.4	74.3	74.3	74.3	73.9	73.4
311.8	310	309.8	309.8	308.8	308.8	308.8	308.4	306	305.8	304.2	303.8	302.4	302	302	302	299	299	298.8	297.8	295	293.2	292.6	288.4	287.8	287.4	287.4	287.4	285.8	284
16	11	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37		39	40	41	42	43	44	45
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APPLICANT: REFF, Mitchell E.
KLOSTZER, William S.
NAKAMURA, Takehiko.
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
ANTIBODIES AND USE THEREOF AS THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
STREET: P.O. BOX 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ver

CURRENT APPLICATION DATA:

APPLICATION UNMERS: US/99/019,441

FILING DATE: 05-Peb-1998

CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                         Sequence 3, Application US/09019441 Publication No. US20030086921A1 GENERAL INFORMATION:
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GENERAL INFORMATION:
ROFF, Mitchell E.
THER OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 THERAPEUTICS
                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                 100.0%; Score 387; DB 11; Length 387; 100.0%; Pred. No. 6e-114; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/103,686
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                                                                                                                                                                                                              LOCATION: 67..387
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 3, Application US/10103686
; Publication No. US20030059424A1
                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
             LENGTH: 387 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                        NAME/KEY: mat_peptide
SEQUENCE CHARACTERISTICS:
                                                                                                                                                      1..387
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                                                                                                                                  NAME/KEY:
                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                        FEATURE:
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61 AGATGTGACATCCAGATGACCCAGTCTCCCTTCTCTGCTCTGCATCTGTAGGGGACAGA 120
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100.0%; Pred. No. 6e-114;
tive 0; Mismatches 0;
               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Serizawa, No. US20030170817Alufusa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 125, Application US/10384933; Publication No. US20030170817A1; GENERAL INFORMATION:
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                               LENGTH: 387 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.0
Matches 387; Conservative
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LENGTH:

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GENERAL INCREMINENT

APPLICANT: Teuji, Takashi

APPLICANT: Teuji, Takashi

APPLICANT: Teuji, Takashi

APPLICANT: Teuji, Takashi

APPLICANT: Teuji, Wasunari

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A

TITLE OF INVENTION: HUMAN MONOCLONAL TRANSDUCTION MOLECULE AILIM AND

TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF

TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF

FILE REPERENCE: 06501-079001

CURRENT APPLICATION NUMBER: US/09/859,053

FRIOR APPLICATION NUMBER: JP 2001-99508

PRIOR APPLICATION NUMBER: JP 2000-147116

PRIOR APPLICATION NUMBER: JP 2000-147116

NUMBER OF SEQ ID NOS: 43

NUMBER OF SEQ ID NOS: 43

SOFTWARE: FastSEQ for Windows Version 4.0
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Gaps
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28; Indels
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Pred. No. 2.6e-
0; Mismatches
Mismatches
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Best Local Similarity 90.7%;
Matches 351; Conservative (
Matches 359; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: sig_peptide
LOCATION: (39)...(104)
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ORGANISM: Homo sapiens
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NAME/KEY: 3'UTR
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NAME/KEY:
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                     CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
PRIOR PILING DATE: EARLIER FILING DATE: 1998-04-01
SEQ ID NOS: 165
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                                                                                                                                                                                                                                                                                             Length 729;
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                                                                                                                                                                                                                                                                                             Score 342.2; DB 13; Length
Pred. No. 1.8e-99;
0; Mismatches 28; Indels
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Pred. No. 1.8e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBLICATION NO. US20030103976A1
GENERAL INFORMATION:
APPLICANT: Serizawa, No. US20030103976A1
APPLICANT: Nakahara, Hideyuki
APPLICANT: Tamahari, Ikuko
APPLICANT: Tamahari, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REPERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT PAPLICATION NUMBER: US/09/499,662
PRIOR PILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/053,583
PRIOR PILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 125
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  CURRENT APPLICATION NUMBER: US/10/384,933
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Publication No. US20030103976A1
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                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 92.8%;
Matches 359; Conservative
                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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; ORGANISM: Homo
US-10-216-484-125
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61 AGAIGIGACATCCAGAIGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
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Sequence 15, Application US/09844684

Patent No. US20020142358A1

GENERAL INFORMATION:

APPLICANT: GEMINI SCIENCE, INC.

APPLICANT: LA JOLLA INSTITUTE FOR ALLERGY AND IMMUNOLOGY

TITLE OF INVENTION: HUMAN ANTI-CD40 ANTIBODIES AND METHODS OF MAKING SAME;

FILE REPERENCE: 21286/0276339

CURRENT APPLICATION NUMBER: US/09/844,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGCTCCTGCTGCTCTCGGCTCTCAGGTACC
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                                                                                                                    Sequence 27, Application US/09905243

Patent No. US200206620041

GENERAL INFORMATION:

APPLICANT: Taylor, Alexander H

TITLE OF INVENTION: Immunogenicity

TITLE OF INVENTION: Immunogenicity

FILE REFERENCE: P50770

CURRENT APPLICATION NUMBER: US/09/905,243

CURRENT FILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: 09/300,970

PRIOR FILING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 97

SOFTWARE: FastSEQ for Windows Version 3.0

FENCINE 100 27
387
                   361 GGCCAAGGGACCAAGGTGGAAATCAAA 387
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Matches 348; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Pan troglodytes
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: (1)...(387)
US-09-905-243-27
                                                                                                                -09-905-243-27
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361
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Publication No. US20030086930A1;
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES;
FILE REFERRICE: PC23019A;
CURRENT FILING DATE: 2002-05-22;
PRIOR APPLICATION NUMBER: 60/293042;
PRIOR APPLICATION NUMBER: 60/293042;
PRIOR FILING DATE: 2001-05-23;
NUMBER OF SEQ 1D NOS: 39;
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 74
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Pred. No. 6.9e-93;
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Patent No. US20020062009A1
GENERAL INFORMATION:
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| GENERAL INFORMATION:
| APPLICANT: KIRIN BER KABUSHIKI KAISHA
| APPLICANT: TAKAHASHI, NOBUZKI
| APPLICANT: TAKAHASHI, NOBUZKI
| APPLICANT: TAKAHASHI, NOBUZKI
| APPLICANT: MIKAYAMA, TOSHIFUMI
| TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBOD
| FILE REFERENCE: 0.21266/0.215601
| CURRENT APPLICATION NUMBER: US/10/040,244
| CURRENT FILING DATE: 2000-4-28
| PRIOR FILING DATE: 2000-4-28
| PRIOR FILING DATE: 2001-04-27
| PRIOR FILING DATE: 2001-04-27
| PRIOR FILING DATE: 2001-04-27
| NUMBER OF SEQ ID NOS: 17
| SEQ ID NO 15
| LENGTH: 728
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89.7%; Pred. No. 2.7e-93;
ive 0; Mismatches 40;
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CURRENT FILING DATE: 2001-04-27
PRIOR PAPLICATION NUMBER: US 60/200,601
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 15
SSPTWARE: PREENTIN Ver. 2.1
SEQ ID NO 15
LENGTH: 728
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; Sequence 15, Application US/10040244
; Publication No. US20030059427A1
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Best Local Similarity 89.7
Matches 347; Conservative
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ORGANISM: Homo sapiens
US-09-844-684-15
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; ORGANISM: Homo sapiens
US-10-040-244-15
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Best Local Similarity
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61 AGATGTGACATCCAGATGACCCCAGTCTCCCTGTCTGCATCTGTAGGGGACAGA 120
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                                                                                                                                                                                                                                                                    APPLICANT: Secrist, Heather
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Secrist, Margarita
APPLICANT: Smith, Carole L.
APPLICANT: Smith, Carole L.
APPLICANT: Scolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.563
CURRENT FILING DATE: 2002-01-31
NUMBER OF SEQ ID NOS: 3417
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 15; Length 537;
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89.4%; Pred. No. 7.8e-93;
iive 0; Mismatches 41
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372 GGCCAAGGACCAAGGTGGACATCAAA 398
                                                                                                                 Sequence 186, Application US/10066543 Publication No. US20030087818A1 GENERAL INFORMATION:
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US-09-844-684-13
; Sequence 13, Application US/09844684
                                                                                                                                                                        APPLICANT: Jiang, Yuqiu
APPLICANT: Pyle, Ruth A.
APPLICANT: Xu, Jiangchun
APPLICANT: Indirias, Carol Yoseph
APPLICANT: Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-186
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Best Local Similarity 89.4'
Matches 346; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 537
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                                                                                 241 CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAGCTG 300
                                                                                                                       301 CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC 360
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APPLICANT: Indirias, Carol Yoseph
APPLICANT: Indirias, Carol Yoseph
APPLICANT: Indirias, Carol Yoseph
APPLICANT: Secriet, Heather
APPLICANT: Carter, Darrick
APPLICANT: Smith, Carole L.
APPLICANT: Smith, John Margarita
APPLICANT: Durham, Margarita
APPLICANT: Stolk, John M.
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.563
CURRENT APPLICATION NUMBER: US/10/066,543
CURRENT FILING DATE: 2002-01-31
NUMBER OF SEQ ID NOS: 3417
SOFFWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 2025
LENGTH: 514
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Pred. No. 7.7e-93;
0; Mismatches 41
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Best Local Similarity 89.4%;
Matches 346; Conservative
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APPLICANT: Pyle, Ruth A.
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CORGANISM: Homo sapiens
US-10-066-543-2025
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Sequence 11, Application US/09844684

Fatent No. US2002042358A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GENINI SCIENCE, INC.
TITLE OF INVENTION: HUMAN ANTI-CD40 ANTIBODIES AND METHODS OF MAKING SAME
TITLE OF INVENTION: HUMAN ANTI-CD40 ANTIBODIES AND METHODS OF MAKING SAME
CURRENT APPLICATION NUMBER: US/09/844,684

CURRENT FILING DATE: 2001-04-27

FRIOR PELLING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PARCHIN Ver. 2.1

SEQ ID NO 11

LENGTH: 698
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Pred. No. 8.7e-93;
0; Mismatches 41; Indels 0;
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Pred. No. 1e-89;
0; Mismatches 47; 1
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Best Local Similarity 87.9%;
Matches 340; Conservative (
                                                                                                                                                                             Query Match
Best Local Similarity 89.4'
Matches 346; Conservative
                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-244-13
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; ORGANISM: Homo sapiens
US-09-844-684-11
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                             LENGTH: 716
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Sequence 13, Application US/10040244

Publication No. US20030059427A1

GENERAL INFORMATION:
APPLICANT: KIRIN BEER KABUSHIKI KAISHA
APPLICANT: TAKAHASHI, NOBURKI
TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBOD
FILE REFERENCE: 021286/0275501
CURRENT APPLICATION NUMBER: US/10/040,244
CURRENT APPLICATION NUMBER: 60/200,601
PRIOR PELING DATE: 2000-4-28
PRIOR PELICATION NUMBER: 60/200,601
PRIOR PELING DATE: 2001-04-27
PRIOR PELING DATE: 2001-04-27
PRIOR PELING DATE: 2001-04-27

NUMBER OF SEQ ID NOS: 17

SOFTWARE PELING DATE: 2010-04-27

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 13
GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: GEMINI SCIENCE, INC.

APPLICANT: LA JOLLA INSTITUTE FOR ALLERGY AND IMMUNOLOGY

TITLE OF INVENTION: HUMAN MATI-CD40 ANTIBODIES AND METHODS OF MAKING SAME

FILE REFERENCE: 21286/0276339

CURRENT APPLICATION NUMBER: US/09/844,684

CURRENT FILING DATE: 2000-04-28

FILOR APPLICATION NUMBER: US 60/200,601

FRIOR PILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.1

LENGTH: 716
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89.4%; Pred. No. 8.7e-93;
ive 0; Mismatches 41; 1
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Best Local Similarity 89.4
Matches 346; Conservative
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US-10-040-244-13
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Search completed: December 30, 2003, 03:42:14
Job time: 563.115 86c8

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Sequence Sequence Sequence Sequence

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Scoring table:

Searched:

Database

Perfect score: Sequence:

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PAPELICANT: NEFF, Mitchell E.
APPLICANT: REFF, Mitchell E.
APPLICANT: REFF, Mitchell E.
APPLICANT: REFF, Mitchell E.
APPLICANT: RACOTERE WILLIAM S.
APPLICANT: NAKAMURA, TAKENIKO
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSER: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: Alexandria
STRATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER: IBM PC compatible
COMPUTER: DATE: DOPPY MISK
COMPUTER: DATE: DOPPY MISK
COMPUTER: DATE: 10-F0-F0-1997
CLASSIFICATION NUMBER: US/08/803;085
FILING DATE: 20-F0-F0-1997
MANDER ATTORNEY/AGENT INPORMATION:
ANDER ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 387
                                                                        US-09-335-697B-18
US-09-335-697B-18
US-09-345-697B-18
US-08-621-751A-5
US-09-620-405B-187
US-09-339-338-187
US-09-433-826B-187
US-09-433-826B-187
US-09-431-826B-187
US-09-431-826B-187
US-09-644-287A-187
                                                                                                                                                                                                                                                                                                                                                                                      US-09-240-274-218
US-09-240-274-221
US-09-240-274-222
US-08-836-561-70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Teskin, Robin L.
REGISTRATION VIMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353.
TELECOMUNICATION INFORMATION:
TELEPRONE: (703) 836-6620
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08803085
Patent No. 6011138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 1...
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; LOCATION:
US-08-803-085-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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206, App
4, Appli
1, Appli
                                                                                                                                                                          December 29, 2003, 16:08:50 ; Search time 42.5992 Seconds (without alignments) 4009.823 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                             1 ATGGACATGAGGGTCCCCGC......GGACCAAGGTGGAAATCAAA 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2 6/ptodata/2/ina/5A_COMB.seq:*
/cgn2 6/ptodata/2/ina/5B_COMB.seq:*
/cgn2 6/ptodata/2/ina/6A_COMB.seq:*
/cgn2 6/ptodata/2/ina/6B_COMB.seq:*
/cgn2 6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2 6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     569978 seqs, 220691566 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                    OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length DB
                                                                                                                                                                                                                                                                                                        US-09-019-441-3
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387 318.2 318.2 316.6 308.6

SO.

Result

304.2 304.2 304.2 304.2 304.2 304.2 304.2

296.2 296.2 296.2 279.4 278.2

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CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC 360
                                                                                                                                                              CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-042-353-358

Sequence 3158, Application US/09042353

Patent No. 6255458

GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
TITLE OF INVENTION:
Producing Heterologous Antibodies
TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIPICATION: 800
                                                                                                                                                                                                                                                                                                                                                             361 GGCCAAGGGACCAAGGTGGAAATCAAA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLUASIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-UUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
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03-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US 08/096,762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/155,301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 22-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-NOV-1993
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 03-DEC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: BARNET, RICHARD S.
APPLICANT: BARNET, RICHARD S.
APPLICANT: BARNET, RICHARD S.
APPLICANT: BARNET, RICHARD S.
TITLE OF INVENTION: MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
FILE REPERENCE: 037003-0275807
CURRENT FILING DATE: 1999-06-30
FRIOR FILING DATE: 1999-06-30
FRIOR FILING DATE: 1999-02-13
FRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 3
SEQ ID NO 3
LENGTH: 19040
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                                                                                              1 Argeacardaggreececencagerecrossecreerecrected
                                                                                                                                                                                                                                                                                                               AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGGTC
                                                               1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGCC
                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA OTHER INFORMATION: referred to as "Mandy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
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                 Indels
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100.0%; Pred. No. 8.8e-113;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 GGCCAAGGGACCAAGGTGGAAATCAAA 387
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Patent No. 6413777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
Best Local Similarity 100.
Matches 387; Conservative
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Best Local Similarity
Matches 387; Conserv
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US-09-343-485A-3
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US-09-343-485A-3
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61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA
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                                                                                                                                       Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LL:
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 014643-009030US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.2%; Score 318.2; DB 4
88.9%; Pred. No. 4.6e-91;
ive 0; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,332
FILING DATE: 07-DCC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/758,417A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/165,699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/728,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 206: US-08-758-417A-206
                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94111-3834
COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                 APPLICANT: Lonberg, Nils
Kay, Robert M.
TITLE OF INVENTION: Transgenic No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Serafini, Andrew T. REGISTRATION NUMBER: 41,303
Sequence 206, Application US/08758417A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 02-Dec-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            576-0300
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
                                                                                                                                                                                                   NUMBER OF SEQUENCES: 417
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Best Local Similarity 88.9
Matches 344; Conservative
                              Patent No. 6300129
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REGISCOPOCKET NUMBER: 014643-009040US
TREECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                      PFILING DATA: 1974
PRIOR PAPLICATION DATA: 372
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA: BAPPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA: WO PCT/US96/16433
FILING DATE: 02-DEC-1996
PRIOR APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
APPLICATION NUMBER: US 08/758,417
FILING DATE: 01-DEC-1997
APPLICATION NUMBER: WO PCT/US97/21803
APPLICATION NUMBER: WO PCT/US97/21803
ATPLING DATE: 01-DEC-1997
ANDME: APPLICATION NUMBER: WO PCT/US97/21803
ATPLING DATE: 01-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.2%; Score 318.2;
88.9%; Pred. No. 4.6
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                                                            JMBER: US 08/209,741
09-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 388 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 88.9
Matches 344; Conservative
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US-08-758-417A-206
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33 ATGGACATGAGGGTCCCGGCTCAGGGCTCCTGGGGCTCTCTGGTTCCCAGGTGCC 92
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APPLICANT: LAKE, PHILIP
APPLICANT: OSTBERG, LARS
TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie ar
                                                                                                                                                                                                                                                                                                                                                                                                                                 393 GGCGGAGGACCAAGGTGGAGATCAAA 419
                                                                                                                                                                                                                                                                                                                                                                                                            361 GGCCAAGGGACCAAGGTGGAAATCAAA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Willam M
REGISTRATION NUMBER: 30,223
TELECOMMUNICATION INFORMATION:
TELEFRONE: (415) 326-2400
TELEFRONE: (415) 326-2420
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08217918
Patent No. 5506132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 387 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
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US-08-217-918-1
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                                                                                                                                                                CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
                                                                                                                                                                                                 241 ccarcaagerrcagcggcagrggarcrggacagarrrcacrcrcaccarcagcagcrg 300
                                                                                                                                                                                                                                     CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC 360
                           GTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 180
                                                         Greacearcactricaceseceaercaesararraecaecrestraecrestarcaecar 180
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APPLICANT: KURIHARA, TATSUYA
APPLICANT: KURIHARA, TATSUYA
APPLICANT: MASSUKURA, SHIGERAZU
APPLICANT: TSURUOKA, NOBUO
APPLICANT: ARIMA, KENJI
APPLICANT: NISHIHARA, TATSURO
TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
TITLE OF INVENTION: PLASMIDS THEREFOR
NUMBER OF SEQUENCES: 9
CORRESPEDIDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
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Pred. No. 2.2e-
0; Mismatches
                                                                                                                                                                                                                                                                                                          GGCCAAGGGACCAAGGTGGAAATCAAA 387
                                                                                                                                                                                                                                                                                                                              GGCCAGGGACCAAGCTGGAGATCAAA 387
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NAME: TITUS, MARLANA K
REGISTRATION NUMBER: 3843
REFERENCE/DOCKET NUMBER: 943:
TELECPHONICATION INFORMATION:
TELEPHONE: 202-861-3711
TELEPHONE: 202-822-0944
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88.6%;
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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nucleic acid
EDNESS: single
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Best Local Similarity 88.6
Matches 343; Conservative
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COUNTRY: US
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61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
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                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,918
FILING DATE: 24-MAR-1994
CLASSIFICATION: 530
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APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
Length 387;
                                           Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
REPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 17-DEC-1991
Score 308.6; DB 1;
Pred. No. 4.9e-88;
0; Mismatches 49;
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PRIOR APPLICATION DATA: APPLICATION NATA:
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28-09-042-353-360
; Sequence 360, Application US/09042353
; Patent No. 6255458
  79.78;
87.38;
                    Best Local Similarity 87.3
Matches 338; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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ZIP: 94111-3834
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61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
PILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION NUMBER:
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APPLICATION NUMBER: US 08/758,417
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION NUMBER: US 08/352,322
APPLICATION NUMBER: US 08/352,322
                                                                                                                                                                                                                          FILING DATE: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION:
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FILING DATE: 03-DEC-1993
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 36(
SEQUENCE CHARACTERISTICS:
                                                                                                                                               FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
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ATTORNEY/AGENT INFORMATION:
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TYPE: nucleic acid
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Matches 337; Conservative
FILING DATE: 26-APR-:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
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APPLICANT: BRAMS, Peter
APPLICANT: BRAMS, Peter
APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: PALSH, Edward E.
APPLICANT: HEARD, Cheryl Janne
APPLICANT: HEARD, Cheryl Janne
APPLICANT: NEWMAN, Roland Anthony
TITLE OF INVENTION: MOUCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
                                                                                                                                                                                                                                                                                       61 agargregacarccagargacccagrerccarccreactererecarcreragaagacaga 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
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                                                                                                                                                                                                                                                                                                                                           GTCACCATCACTTGCAGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG 180
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                                           Length 439;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,376
                                                                                                                                               1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTJ
                                           Score 307; DB 4;
Pred. No. 1.7e-87;
0; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Burns, Doane, Swecker & Mathis P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 GGCCAAGGGACCAAGGTGGAAATCAAA 387
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FILING DATE: 07-UN-1995
CLASSIFICATION: 42
ATORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/08488376 Patent No. 5811524
                                              79.3%;
87.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                 Conservative
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                                                                     Best Local Similarity
Matches 337; Conserv
US-08-758-417A-208
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                                                   Query Match
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                                                   CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC 360
                                                                                               301 caeccreaagarrrrecaacrrarracreccaacagrargaracrecceracacrrrr 360
241 CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG 300
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lonberg, Nils
Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing Heterologous Autibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: O2-Dec-1996
CLASSIFICATION: <u >un cunknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend and Crew LL
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRADICATION NUMBER: US 08/728,463
FILING DATE: 10-CT-1996
APPLICATION NUMBER: US 08/54,404
FILING DATE: 10-CT-1995
APPLICATION NUMBER: US 08/35,322
FILING DATE: 0-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 09-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/165,699
FILING DATE: 12-JUL-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 12-JUL-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 12-JUL-1993
APPLICATION NUMBER: US 08/055,311
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/055,311
FILING DATE: 22-AUL-1993
APPLICATION NUMBER: US 08/053,331
FILING DATE: 26-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
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SEQUENCE DESCRIPTION: SEQ ID NO: 208:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                    GGCCAAGGGACCAAGGTGGAAATCAAA 387
                                                                                                                                                                                   Sequence 208, Application US/08758417A Patent No. 6300129 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 439 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 208
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
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US-08-634-224-16
| Sequence 16, Application US/08634224
| Sequence 16, Application US/08634224
| Patent No. 5866125
| GENERAL INFORMATION:
| APPLICANT: BRAMS, Peter |
| APPLICANT: CHAMAT, Soulaima Salim |
| APPLICANT: MALSH, Edward E. |
| APPLICANT: WALSH, Edward E. |
| APPLICANT: WEWAN, Roland Anthony |
| TITLE OF INVENTION: WEUTRALIZING HIGH AFFINITY HUMAN |
| TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF |
| NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 GACATCCAGATGACCCAGTCTCCCTTCTCCTGCATCTGTAGGGGACAGAGTCACC 126
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87.4%; Pred. No. 1.5e-86;
tive 0; Mismatches 48
                                                                                                                                                                                                      NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELECOMINICATION INFORMATION:
TELEPRINE: (703) 836-6620
ITELEPRIONE: (703) 836-2021
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
US/08/634,223
                                                                                                                         US/08/488,376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                      CLASSIFICATION:
PAROR APPLICATION DATA:
APPLICATION UNMER: US/0:
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 705 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 333; Conservative
   APPLICATION NUMBER:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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APPLICANT: BRAMS, Peter
APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: PAN, Li-Zhen
APPLICANT: PAN, Li-Zhen
APPLICANT: PAN, Li-Zhen
APPLICANT: PAN, Li-Zhen
APPLICANT: NEWMAN, Roland Anthony
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & MOLL
CORRESPONDENCE ADDRESSEE: BURNS, DOANE, SWECKER & MOLL
CORRESPONDENCE ADDRESSEE: BURNS, DOANE, SWECKER & MOLL
CORRESPONDENCE ADDRESSEE: BURNS, DOANE, SWECKER & MOLL
CORRESPONDENCE ADDRESSEE: BURNS, DOANE, SWECKER & MOLL
CORRESPONDENCE ADDRESSEE: BURNS, DOANE, SWECKER & MOLL
CORRESPONDENCE ADDRESSEE: BURNS, DOANE, SWECKER & MOLL
CORRESPONDENCE ADDRESSEE: BURNS, DOANE, SWECKER & MOLL
CORRESPONDENCE
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                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 705;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      Score 304.2; DB 1
Pred. No. 1.5e-86;
0; Mismatches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 GGGACCAAGGTGGAAATCAAA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGACCAAGGTGGAAATCAAA 381
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Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: BRAMS, Peter
                            SEQUENCE CHARACTERISTICS:
LENGTH: 705 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOCY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 87.4%;
Matches 333; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Virginia
COUNTRY: United States
   INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                1..705
                                                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: 1...7
US-08-488-376-16
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US-08-634-223-16
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240 306 366

120 186 180

9

Gaps

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Sequence 16, Application US/08634400 Patent No. 5939068 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 705 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 87.4 Matches 333; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-634-400-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GGGAAAGCCCCTAAGCTCCTGATATATGCTGGATCCAATTTGCACCGTGGGGTCCCGTCA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 AGGTTCAGTGGCGGTGGATCTGGGACAGATTTCACTCTCACCATCAACAGTCTGCAACCT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307 GAAGATTTTGCGACTTATTACTGTTTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAA 366
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                                                                                    CITY: Alexandia
STATE: Virginia
COUNTRY: United States
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,224
FILING DATE: US/08/631,224
FILING DATE: US/08/631,224
FILING DATE: US/08/100: 150
ATPORNEY/AGENT INFORMATION:
NAME: TEASIN NUMBER: US/08/620
TELECOMMUTICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELECOMMUTICATION INFORMATION:
TELEPHONE: (703) 836-620
TELECOMMUTICATION INFORMATION:
TYPE: INCOLETION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
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87.4%; Pred. No. 1.5e-86;
iive 0; Mismatches 48
                                 ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 78.6
Best Local Similarity 87.4
Matches 333; Conservative
            CORRESPONDENCE ADDRESS:
                                                                     CITY: Alexandria
STATE: Virginia
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LOCATION:
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US-08-634-224-16
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RESULT 12 US-08-634-400-16

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APPLICANT: BRAMS, Peter
APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: PAN, Li-Zhan
APPLICANT: PAN, Li-Zhan
APPLICANT: PAN, Li-Zhan
APPLICANT: HEARD, Cheryl Janne
APPLICANT: NEWMAN, ROLTALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: BUTTE, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126
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                                                                                                                                                                                                                                                                                                                          CUTY: Alexandria
STATE: Virginia
STATE: Virginia
COUNTRY: United States
ZIB: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,400
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87.4%; Pred. No. 1.5e-86;
:ive 0; Mismatches 48;
                                                                                                                                                                                                                                                                                 ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/488,376
FILING DATE: 07-JUN-1995
ATTORNEY AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
FEFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-620
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 base pairs
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APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: PAN, Li-Zhen
APPLICANT: MALSH, Edward E.
APPLICANT: HEARD, Chertyl Janne
APPLICANT: NEWMAN, Roland Anthony
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
TITLE OF INVENTION: MATHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
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61 GACATCCAGATGACCCAGTCTCCATCCTCCTGTCTGCTGTGGGAGACAGAGTCACC 120
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                                                                                                                                                   307 GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAA 366
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                                                                                                      127 ATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAGAAACCA
                                                                                                                                                                                                                                           187 GGAAAAGCTCCTAAGCTCCTGATCTAGCTCCAGTTTGCAAAGTGGGGTCCCATCA
                                                                                                                                                                                                                                                                                                       181 GGGAAAGCCCCTAAGCTCCTGATATATGCTGGATCCAATTTGCACCGTGGGGTCCGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria STATE: Virginia COUNTRY: United States
ZIP: 22313-1404
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IB
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/488,376
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367 GGGACCAAGGTGGAAATCAAA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 GGGACCAAGGTGGAAATCAAA 381
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Patent No. 5958765
GENERAL INFORMATION:
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REGISTRATION NUMBER: 35,030
REPERENCE/DOCKET NUMBER: 012
TELECOMMUNICATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
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TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 705 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: |
FEATURE:
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US-08-770-057-16
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APPLICANT: CHAMAY, Soulaima Salim
APPLICANT: PAN, Li-Zhen
APPLICANT: WALSH, Edward E.
APPLICANT: WEEKH, Edward E.
APPLICANT: NEWMAN, Roland Anthony
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSES: BUTTA, Doane, Swecker & Mathis
STREET: P.O. BOX 1404
CITY: Alexandria
                                                                             GAAGATITICCGACTIATIACIGICIACAGGITITAIAGIACCCCTCGGACGITCGGCCAA 366
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          241 AGGTTCAGTGGCGGTGGATCTGGGACAGATTTCACTCTCACCATCAACAGTCTGCAACCT 300
                                                                                                                                            301 GAAGATTTTGCAACTTACTATTGTCAACAGGCTTACAGTACCCCCTGGACTTTCGGCCCA
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/635,878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,376
FILING DATE: 07-UNH-1995
ATTORNEY AGENT INFORMATION:
NAME: TEGKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
REFERENCE/DOCKET NUMBER: 012712-150
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-620
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
LENGTH: 705 base pairs
TYPE: NUCleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                               GGGACCAAGGTGGAAATCAAA 387
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Best Local Similarity 87.4%;
Matches 333; Conservative
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STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
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; LOCATION:
US-08-635-878-16
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Length 705; Indels 9

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       REFERENCE FOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHRACTERISTICS:
LENGTH: 705 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                    Score 304.2; DB 3
Pred. No. 1.5e-86;
0; Mismatches 48
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; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-335-6978-16
                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 87.4%;
Matches 333; Conservative
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HEARD, Cheryl Janne
NEWMAN, Roland Anthony
INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
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                                                                                                                                                                                                                                                                                                     ATCACTTGCAGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAGAAACCA 186
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                                                                                                                                                                      1 ATGGAGACCCCTGCTCAGCTCCTGGGCTCCTGCTACTCTGGCTCCGAGGTGCCAGATGT 60
                                                                                                                                                7 ATGAGGETCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGCCAGATGT
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                                                                      Length 705;
                                                                                                           48; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
                                                                        DB 2;
                                                                      Score 304.2; DB 2
Pred. No. 1.5e-86;
0; Mismatches 48
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APPLICATION NUMBER: US/09/335,697B
FILING DATE: 06-Jul-2000
CLASSIFICATION: <Unknown>
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APPLICATION NUMBER: 08/770,057
FILING DATE: <Unknown>
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CHAMAT, Soulaima Salim
PAN, Li-Zhen
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                                                                        78.6%;
87.4%;
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CORRESPONDENCE ADDRESS:
                                                                                                           Conservative
                                                                                         al Similarity
333; Conserv
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US-09-335-697B-16
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 ; NAME/KEY:
; LOCATION:
US-08-770-057-16
NAME/KEY:
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December 29, 2003, 16:08:50 ; Search time 1379.44 Seconds (without alignments) 9875.644 Million cell updates/sec
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333
1_CAGTCTGCCCGACTCAGCC......CCCGGTTGACCGTCCTAGGT 333
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                      OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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em_sv:*
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Maximum DB seq length: 200000000
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ggb_ntg:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RIES	Description	*******************	Z85043 H.sapie	AB064155 Homo sa	L03632 Human IG	285033	M75282 Human Ig	M75139 Human I	AB064152 Homo	ABU64164 HOMO	ABU64024 HOMO	AB064163 Homo	AB064000 Homo	.285382	Z85358 H. sapie	043/72 Human 1	AB064153 Homo	AJ006162	AF194592 Homo	AF194604 Homo	X9573	AB064	28535	AX3/9 AB064	AF194	AF194586 Homo sapi	AF194	AFI34	AF194	X7274	1994 1994	AF43	28503	Z85297 H.sapie	AU249377 AX703432	AX703435 Seque	AF194595	AFLY4603 HOMO SAP AF194607 HOMO SAD	Z84836 H.sapiens	MENTS	01 444 30 444	bp DNA linear PRI 06-FEB-199 in variable region gene	ıt-Lambda;	mmunodlobulin	earranged; variable region.	ata: Ve	Catarrhini; Hominidae;	., Jones, P.T. and Winter, G.
SUMMARIES	GI .		HSZ85043	AB064155	HUMIGLAD	HSZ85033	HUMIGLDS	HUMIGLVD:	AB064152	AB064164	AB064024	AB064163	AB064000	HSZ85382	HSZ85358	HS043772	AB064153	HSA00616	AF194592	AF194604	HSIGLCVR	AB064020	HSZ85355	AX379222	AF194579	AF194586	AF194587	AF194589	AF194608	HSRIGLVC	HSU76676	AF45318	HSZ85035	HSZ85297	AX703432	AX703435	AF194595	AF194603	HSZ84836	ALIGNMENTS			rearranged; I	I:1834754	family, r	Chordata.	Primates;	Tomlinson, I.M.
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	% Query Match	1	œ.	α	~	^	~	^	^	r (	- 1		· w	9	vo 1	9	o w	9	v	·ω	oν	9	9	9	o un	85.6	S C	U U	J LO	S	S t	n u	N I	un i	വ	S (C)	S I	n u	J FU			HSZ85043 H.sapiens	-17ITI 043	043.1 igen re	unoglob	o sapie	malia;	gnatovich, O.,
	Score		293	293	291.4	291.4	291.4	291.4	291.4	291.4	283.6	283.08	288.2	288.2	288.2	288.2	288.2	287.8	286.8	286.8	286.6	286.6	286.6	286.6	285.2	285.2	285.2	285.2	285.2	285.2	285	2 8 5 2 8 5	285	285	284.6	284	83	283.6	0 00			Z			immi			н н
	Result No.		rel	~	m	4	S	9	7	ω (	י סיי	0 F	12	13	14	15	17	18	19	50	7 6	23	24	25	27	28	29	9 6	35	33	W (	n 4	37	38	ມ 4 ບັດ	41	45	E 4	4 4		RESULT 1 HSZ85043	LOCUS DEFINITION	ACCESSION	VERSION	a Jan 10's	ORGANISM		REFERENCE

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/translation="MKXLLPTAAAGLLLLAAOPAMAQSALTQPASVSGSPGOSITISC
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CQVTHEGSTVEKTVAPTECSARQSTPFVCEYQGQSSDLPQPPVNAGGGSGG"
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Human IG rearranged lambda-chain mRNA V-J-C-region, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 CACCCAGGCAAAGCCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 TCTAATCGCTTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 306
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/gene="IGD"
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therapeutic human antibodies and application to functional
                                                                                                                   % Z Lucau...
3 Kurosawa,Y.
Direct Submission
L Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyoake 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="AlMS4"
/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 806;
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Prèd. No. 5.6e-75;
0; Mismatches 25; Indels
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214 g 161 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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253 c
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92.5%;
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/gene="IGL"
                                                                                                        (bases 1 to 806)
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Matches 308; Conserv
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ORIGIN
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806 bp mRNA linear PRI 02-JUL-2002
Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
region, partial cds, clone:Ll5.
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Construction and characterization of antibody libraries: isolation
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   KXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CAGTCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATC
                                                                                                                                                                              Direct Submission
Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 20H, UK
Location/Qualifiers
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Pred. No. 5.8e-75;
0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell_type="lymphocyte"
tissue type="peripheral blood"
clone_lib="cDNA library"
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                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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|isolate="donor IT"
|db_xref="taxon:9606"
|map="22411.2"
|clone="24-17ITIIH34"
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/gene="IGLV"
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                                                                  J. Mol. Biol.
2 (bases 1 to 435)
Ignatovich, O.
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PRI 06-FEB-1997
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241 CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTA 300
                         266 CAGGCTGAGGACGAGGCTGATTATTACTGCAGCTCATATACAAGCAGCAGCACTCTGTGGTA 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G. XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (O6-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                 antigen receptor; immunoglobulin; immunoglobulin light chain; immunoglobulin, superfamily; rearranged; variable region.
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H.sapiens Ig lambda light chain variable region gene
(24-071TIIB176) rearranged; Ig-Light-Lambda, VLambda.
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Pred. No. 1.7e-74;
0; Mismatches 26;
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/tissue type="peripheral blood"
/clone lib="cDNA library"
                                                                           301 TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 333
                                                                                                   326 TTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol type="genomic DNA"
/mol type="denor IT"
/db xxef="taxon:9606"
/map="22411.2"
/clone="24-07ITIB176"
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larity 92.2%;
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Homo sapiens
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2 (bases 1 to 435)
Ignatovich, O.
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/db_xref="G1:186091"
/db_xref="G1:186091"
/db_xref="GD8:G00-128-432"
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WYQQHPGKAPRLMYDVSNRPSGSVSNRPSGSKSGNTASLTISGLQAEDEADYYCSSYT
SSSSVVFGGGTKLTVLGQPKAAPSVTLFPPSSEE"
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                                       J-region; V-region; immunoglobulin lambda; immunoglobulin
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                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.

Mammalia; Eutheria; Primates; Catarrhini, Hominidae, Homo.

Man, Catarrhini, Homo.

Paul, E., Iliev, A., Livneh, A. and Diamond, B.

The anti-DNA associated idiotype 8.12 is encoded by the V lambda III gene family and maps to the vicinity of L chain CDR1

J. Immunol. (1992) In press

Original source text: Homo sapiens (individual_isolate SLE patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 CACCCCAGGCAAAGCCCCCAAAACTCATGATTATGATGTCAGTAATGGCCCTCAGGGGTT 205
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codon_start=2
product="immunoglobulin lambda-chain"
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Pred. No. 1.7e-74;
0; Mismatches 26;
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                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol type="mkNA"
/isolate="SLE patient PV"
/db xref="taxon:9606"
/map="22q11.1-q11.2"
/call type="B lymphocyte"
/ call type="IGL@"
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/gene="IGL@"
/note="G00-128-432"
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133 c 103 g
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                                         C-region; J-region; V-regior
light chain; processed gene.
Homo sapiens (human)
Homo sapiens
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92.2%;
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הטיווטבעטטא 473 bp mRNA linear PRI 05-JAN-1995
Human Ig rearranged lambda chain (V-lambda-2.DS) mRNA, V-, J-, and
C-region gubgroup II.
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Paul, B., Livneh, A., Manheimer-Lory, A.J. and Diamond, B.
Characterization of the human Ig V lambda II gene family and characterization of the human Ig V lambda II gene family and charalysis of V lambda II and C lambda polymorphism in systemic lupus
                                                                                                                                   267 TCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 326
                                                                                                                                                                                                       CAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTA 300
147 TCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAG 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         M75139.1 GI:186154
C-region; J-region; V-region; immunoglobulin; immunoglobulin
lambda; immunoglobulin light chain; variable region subgroup II.
                                                          CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC
                                                                                                             TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
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DEADYYCSSYTSSSTFVFGGGTKLTVLGQPKAAPSVTLFPPSSEEL"
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'translation="MAWALLLLTLTQGTGSWAQSALTQPASVSGSPGQSITISCTGT
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Paul, E., Livrah, A., Manheimer-Lory, A. and Diamond, B. Characterization of the human immunoglobulin V-lambda-II gene family and analysis of V-lambda-II and C-lambda polymorphism in systemic lupus erythematosus J. Immunol. (1991) In press
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/cell_line="EBV-transformed B cell"
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/mol type="mRNA"
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Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
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CQVTHBGSTVEKTVAPTECSARQSTPFVCEYQGQSSDLPQPPVNAGGGSGG"
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Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
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Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University, Kutsukake-cho, Toyoke 470-1192, Japan (B-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387) Please visit our web site URL:http://www.fujita-hu.ac.jp/immunity/.
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TGTSSDVGGYNYVSWYQQHPGKAPKLMIYDVSKRPSGVSNRFSGSKSGNTASLTISGL
QAKDEADXYCSSYTSSSTWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVÇ
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Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
  TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120
                                                                                                                                         CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC 180
                                                                                                                                                                 TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 240
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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'protein id="BAC01780.1"
'db_xref="GI:21669511"
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/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
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Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyoake 470-1192, Japan (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
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Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/gene="IGL"
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/trānslation="QSALTQPASVSGSPGQS1T1SCTGTSSDVGGYNYVSWYQQHPGK
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Homo sapiens partial mRNA for thyroid peroxidase-specific
immunoglobulin lambda chain variable region (IGLV gene), clone Bl0.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="immunoglobulin lambda light chain VLJ region"
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/db_xref="G1:21669255"
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/db_xref="taxon:9606"
/clone="L153"
/clone="L153"
/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
  Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyoake 470-1192, Japan (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387) Please visit our web site URL:http://www.fujita-hu.ac.jp/immunity/.
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/organism="Homo sapiens"
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/gene="IGL"
/codon_start=1
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TGTSSDVGGYNYVSNYQQHPGKAPELMIYDVSKRPSGVSNTRFGSKSGNTASLTISGL
ABDBADYYCSSYTGSSTHWYPGGGFKLTVLGQPKAAPSVTLFPPSSELQANKATLVC
LISDPYPGAVTVAWRADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYS
CQVTHEGSTVEKTVAPTECSARQSTPFVCEXQGGSSDLPQPPVNAGGGSGG"
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Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                          product="immunoglobulin lambda light chain VLJ region"
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/db_xref="GI:21669535"
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region, partial cds, clone:L153.
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/note="mixture of tissues:tonsils, umbilical cords, peripheral blood and bone marrow"
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Pred. No. 1.7e-74;
0; Mismatches 26;
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al Similarity 92.2%;
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/gene="IGL"
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PRI 14-DEC-2001

DEFINITION

RESULT 9 AB064024

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

REFERENCE AUTHORS TITLE

JOURNAL

TITLE

240

9 9

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PRI 02-JUL-2002

linear

mRNA

810 bp

AB064163

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Thyroid peroxidase autoantibodies obtained from random single chain FV libraries contain the same heavy/light chain combinations as
                                                                                                                                                                                                                                                                                                                                                                                                            note="Anti-thyroid peroxidase scFv fragment isolated from phage display combinatorial library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /trānslation="QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGK
APKLMIYDVSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTSSSTRVFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACCCAAAGCCCCCCAAACTCATGATTTATGATGTCAGTAATCGGCCCTCAGGGGTT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CAGTCTGCCCTGACTCAGCCTGCCTCGTGTCTGGGTCTCCTGGACAGTCGATCACCATC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="immunoglobulin lambda chain variable region"
                                                                                                                           Chapal, N.
Chapal, N.
Direct Submission
Submitted (05-JAN-2000) Chapal N., Faculte de Pharmacie, CNRS
UMR9921, 15 avenue Charles Flahault, Montpellier 34060, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="immunoglobulin lambda chain variable region"
102 c 84 g 78 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGTCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGGTCTCCTGGACAGTCGGTCACCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 333;
                                                                                                                                                                                                                                                                                                                                     cell_type="Thyroid infiltrating B cells"
clone_lib="panB library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 289.8; DB 9;
Pred. No. 5.1e-74;
0; Mismatches 27;
                                                                       Endocrinology 142 (11), 4740-4750 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAC06678.1"
/db_xref="GI:9968428"
/db_xref="REMTREMBL:CAC06678"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCGCCGAGGACCAAGCTGACCGTCCTAGGT
                                                                                                                                                                                                                                                             organism="Homo sapiens"
Bouanani, M. and Peraldi-Roux, S.
                                                                                                                                                                                                                                                                                                  db_xref="taxon:9606"
clone="B10"
                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             country="France"
                                                                                                                                                                                                                                                                                 mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="IGLV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="IGLV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="IGLV"
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                                                          occur in vivo
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Matches 306
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AUTHORS
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RESULT 11 AB064163

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/translation="MKYLLPTAAAGLLLLAAQPAMAQSALTQPASVSGSPGQSITISC
TGTSSDVGGTWTVSWYQQHECKAPKLMTYDVSKREGGVSRESGSKGNTASLTISGL
QAEDEADYTCSSYTSSSSWYCGGGTKTTULQQPKAAPSVTLPPPSSEELQANKATLVC
LISDFYPGAVTVAMKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHKSYS
CQVTHEGSTVEKTVAPTECSARQSTPFVCEYQGQSSDLPQPPVNAGGGSGG"
                                                                                                                                                                                                                                                                                                                                                                            Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M., Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J., Multa,K. and Kurosawa,Y.
Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                       Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/product="immunoglobulin lambda light chain VLJ region"
/protein id="BAC01791.1"
/db_xref="GI:21669533"
Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ region, partial cds, clone:L23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGCCTCCCTGACCATCTCTGGGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="AIMS4"
/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyoake 470-1192, Japan (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387) Please visit our web site URL:http://www.fujita-hu.ac.jp/immunity/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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0; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="pelB signal peptide"
254 c 215 g 164 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                        AB064163.1 GI:21669532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="L23"
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ilarity 91.9%;
Conservative
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/gene="IGL"
                                                                                                                                                                                                  Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l. .66
/gene="IGL"
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Unpublished
2 (bases 1 to 810)
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hes 306; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kurosawa, Y.
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               DEFINITION
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AUTHORS
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                                                                                         ACCESSION
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HSZ85382 19 lambda light chain variable region gene (34-09SWIIC37)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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20H, UK
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antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
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Pred. No. 1.5e-73;
0; Mismatches 28;
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/tissue type="peripheral blood"
/clone lib="cDNA library"
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Submitted (06-FEB-1997) Ignatovich O.,
Engineering, Hills Road, Cambridge CB2
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/mol type="genomic DNA"
/isolate="donor SW"
/db xref="taxon:9606"
/map="22q1.2"
/clone="34-09SWIIC37"
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J. Mol. Biol.
2 (bases 1 to 375)
Ignatovich, O.
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Homo sapiens
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/product="immunoglobulin lambda light chain VLJ region"
/protein_id="BAC01628.1"
/db xref="G1:21669207"
/translation="QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGK
APKLMYYDVSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTSSSTYPFG
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Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
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                                                                                                             307 CAGGCTGAGGACGAGGCTGATTATTACTGCAGCTCATATACAAGCAGCAGCTCTTGGGT 366
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         247 TCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 306
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
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Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University;
Kutsukae-cho, Toyoake 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.tujita-hu.ac.jp/immunity/.
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Pred. No. 1.5e-73;
0; Mismatches 28; Indels
                                                                                                                                                                                                                                        367 TTCGGCGGAGGACCAAGCTGACGTCCTAGGT 399
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L129"
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/gene="IGL"
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Kurosawa, Y.
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Human immunoglobulin light chain variable region mRNA, cell line
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SSDVGGYNYVSWYQQHPGKAPKLMIYDVSNRPSGVSNRFSGSKSDNTASLTISGLQAE
DEADYYCSSYTSSSTLVFGGGTKLTVLR"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 453)
Boucher, G., Broly, H. and Lemieux, R.
Restricted Use of Cationic Germline VH Gene Segments in Human Rh(D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (21-DEC-1995) Gerard Boucher, Research and Development, The Canadian Red Cross Society, Transfusion Center of Quebec, 2535 Laurier Boulevard, Ste-Foy, Quebec GIV 4M3, Canada Location/Qualifiers
                                                                                                                                298 CAGGCTGAGGACGCTGATTATTACTGCAGCTCATATACAAGCAGCAGCACTCTCGTC 357
178 CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCAGTAATCGGCCCTCAGGGGTT 237
                                                                                                          241 CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTA 300
                               181 TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
                                                                         238 TCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
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/note="Rhesus blood group antibody V region"
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/product="Ig light chain variable region"
58. .123
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/note="rearranged"
                                                                                                                                                                                      333
                                                                                                                                                                                                       358 TTCGGAACTGGGACCAAGGTAACCGTCCTAGGT 390
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    organism="Homo sapiens"

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/note="encodes FR4"
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/note="encodes CDR1"
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H.sapiens Ig lambda light chain variable region gene (25-28SWIID60)
rearranged; Ig-Light-Lambda; VLambda.
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                     TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 240
                                                                                             181 TCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTCTGGGCTC 240
                                                                                                                                                                      241 CAGGCTGAGGACGCTGATTATTACTGCAGCTCATATACAAGCAGCACCTCTCGTC 300
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                                                                                                                                                   CAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTA 300
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XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Repertoire
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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antigen receptor; immunoglobulin; immunoglobulin light chain; immunoglobulin superfamily; rearranged; variable region. Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="lymphocyte"
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Submitted (06-FEB-1997) Ignatovich O., N
Engineering, Hills Road, Cambridge CB2;
Location/Qualifiers
                                                                                                                                                                                                                           301 TTCGGAAGAGGACCCGGTTGACCGTCCTAGGT 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /moi_type="genomic_DNA"
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/gene="IGLV"
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2 (bases 1 to 435)
Ignatovich,O.
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                                                                  0; Gaps
                                    Query Match

86.5%; Score 288.2; DB 9; bength 453;
Best Local Similarity 91.6%; Pred. No. 1.5e-73;
Matches 305; Conservative 0; Mismatches 28; Indels 0;
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Search completed: December 29, 2003, 19:01:21 Job time : 1380.44 Becs

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BG756493 602715633 BG483745 602503383

BG397282 60243906

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Database

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BE975970 880 bp mRNA linear EST 22-JAN-2001
602246174F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4337226 5',
mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov. c column: 19
High quality sequence stop: 759.
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                                                                                                                                                                                          BG756342
BG756874
BF976229
BG397302
BG754756
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AV686421
BG564971
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BF975970 602246174
BM914350 AGENCOURT
AV694861 AV694861
AV693754 AV693754
                                                                                December 29, 2003, 16:08:50 ; Search time 1440.93 Seconds (without alignments) 5616.780 Million cell updates/sec
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1 CAGTCTGCCCCGACTCAGCC......CCCGGTTGACCGTCCTAGGT 333
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                      22781392 seqs, 12152238056 residues
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Maximum Match 100%
Listing first 45 summaries
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BM914350
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                                                           nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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291.4 285 281.8 281.8

AW404544 UI-HF-BLO BM007694 603617126 BG541853 602569746 AW405058 UI-HF-BLO BG536723 602564852 BQ712542 AGENCOURT

AM406701 UI-HF-BLD BG059377 nab50e11. BG759257 602710315 BG759257 602713013 BG756342 602713013 BG756342 602713013 BG756342 602713062 BG756342 602245104 BG756342 602245104 BG75475 602245104 BG75475 602245104 BG75475 602245104 BG756477 602438617 BG564971 602581343 BG564971 602581343 BG566477 602581343 BG566477 602581343 BG566477 602581343 BG56677 602581361 BG75677 602581361 BG774961 602581363 BM831025 K-ESTO0104 BM831030 K-ESTO0104 BM831098 K-ESTO0104 BM830982 K-ESTO0104 BM830988 K-ESTO057 BM73502 K-ESTO057 BM73502 K-ESTO057 BM73502 K-ESTO057 BM73604 K-ESTO057 BM73604 K-ESTO057

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o mRNA linear EST 16-JAN-2002 clone GKCGWE01 5', mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 710)

1 (bases 1 to 710)
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found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM2002 row: d column: 03 High quality sequence stop: 538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 85.6%; Score 285; DB 12; Best Local Similarity 91.0%; Pred. No. 1.5e-69; Matches 303; Conservative 0; Mismatches 30;
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                                                                                    Location/Qualifiers
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                                                                                                                             /tissue type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clocallb="NTH MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: aGCACGAGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
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NIH-MGC http://mgc.nci.nih.gov/.
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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Pred. No. 2.1e-71;
0; Mismatches 26; Indels
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                                                      organism="Homo sapiens"
                                                                                                                   /clone="IMAGE:4337226"
                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
             Location/Qualifiers
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Homo sapiens
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Best Local Similarity 92.2
Matches 307; Conservative
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요 ò a ò a ò 셤 ð 셤 ò 유

120

180 283

163

9

Gaps

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Length 1078; Indels

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AV697043 AVC Homo sapiens cDNA clone GKCGWG01 5', mRNA sequence.
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1 (bases 1 to 767)

Xu,X.; Huang,J.; Xu,Z., Qian,B.; Zhu,Z., Yan,Q.; Cai,T.; Zhang,X.;
Xiao,H.; Qu,J.; Liu,F.; Huang,Q.; Cheng,Z.; Li,N.; Du,J.; Hu,W.;
Shen,K.; Lu,G.; Fu,G.; Zhong,M.; Xu,S.; Gu,W.; Huang,W.; Zhao,X.;
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
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                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="GKC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                 Contact: Zeguang Han
Contact: Zeguang Han
Contact: Zeguang Han
Contact: Zeguang Han
Shanghai
Jan Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-508019122
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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/dev stäge="Adult"
/lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9;
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Pred. No. 9.9e-69;
0; Mismatches 32
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                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKCGWD05"
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90.4%;
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Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver watch Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                                                                                                                      /dev stage="raduit"
/lab_host="SOLR"
/clone lib="GKC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                Contact: Zeguang Han
Contact: Zeguang Han
Contact: Zeguang Han
Contact: Zeguang Han
J51 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801912
Email: hanzgebng.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 281.8; DB 9;
Pred. No. 9.9e-69;
0; Mismatches 32;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKCGWE01"
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90.4%;
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AV693754
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BX280395 Soares multiple sclerosis 2NbHMSP Homo sapiens cDNA clone IMAGP998B24628 ; IMAGE:283391, mRNĀ sequence.
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1 (bases 1 to 485)
Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B.
Human UnigeneSet - RZPD3
                                                                                                                                                                                                                                                                                                        clone_lib="GKC"
note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                           Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
S15 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
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Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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Pred. No. 1e-68;
Trimination 32; Indels
                                                                                                                                                                                                                                                           Lissue type="hepatocellular carcinoma"
dev stage="Adult"
lab_host="SOLR"
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|organism="Homo sapiens"
                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKCGWG01"
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90.4%;
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Contact: Ina Rolfs
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 301; Conservative
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                                                                                                                                                                                                                                                                               This clone is available royalty-free from RZPD; contact RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissum.trpe="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Sosses multiple_sclerosis_2NbHMSP"
/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not 1; Site_2: Eco
; ist strand_cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC
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                                                         RZPDLIB; I.M.A.G.E. CDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/Cgi-
bin/schowib.pl.cgi/response?libno=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Faz: 449 30 32639 101
Fax: 449 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
  Gabi
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RZPD Deutsches Ressourcenzentrum fuer Genomforschung
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
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Pred. No. 2.3e-68;
0; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="1MAGp998E24628 ; IMAGE:283391"
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                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                RZPD; IMAGD998E24628.
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Best Local Similarity 90.1%;
Matches 300; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
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/organism="Homo sapiens"

/mol_type="mRNA"

/db_txef="lawaon:9606"

/clone="IMAGE:3034479"

/tissue_type="Human Placenta"

/lab_host="DHIHOB TonA"

/clone_lib="NIH MGC_147"

/note="Organ: placenta; Vector: pBluescriptR; Site_1:

/note="Organ: placenta; Vector: pBluescriptR; Note: placenta; Note: placenta; Note: placenta; Note: placenta; No
                          CD101742
AGENCOURT_13902002 NIH MGC_147 Homo sapiens cDNA clone
IMAGE:30347479 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN) and advice from Piero Carninci (RIKEN) and advice from Piero Carninci (RIKEN) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be though the I.M.A.G.E. Consortium/Linn at: http://image.llnl.gov
                                                                                                                                                                                                                                      Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 766)
                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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AV699040 GKC Homo sapiens cDNA clone GKCGXE07 5', mRNA sequence.
AV699040
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I (bases 1 to 751)

Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, H., Ghen, Z. and Han, Z.

Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncencerous liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
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/dev_stage="Adult"
/lab_host="SOLR"
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This clone is available at CHGC in Shanghai.
Location/Qualifiers
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0; Mismatches 33
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/db_xref="taxon:9606"
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Matches 300; Conservative
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DB 14; Length 766;
                                                                Indels
Query Match

84.1%; Score 280.2; DB 14;
Best Local Similarity 90.1%; Pred. No. 2.9e-68;
Matches 300; Conservative 0; Mismatches 33;
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/Gol type="mrkNA"
/ db_xref="taxon:9606"
/ clone="irwARS:15684"
/ lab_host="irwARS:15684"
/ lab_host="irwARS:15684"
/ lab_host="irwARS:15684"
/ lab_host="irwARS:15684"
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/ note="forgan: pooled brain, lung, testis; Vector:
/ note="forgan: pool of 6 male brains, age range 23-27;
/ pcWv-SpoRT6; Site_1: Not!; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age 69. Library is
oligo-for primed and directionally cloned (EcoRV site is
centriched for full-length clones and was constructed by C.
Gruber (Invirogen). Research Genetics tracking code
021. Note: this is a NIH MGC Library."
                                                                                                                                                                                    787 bp mRNA linear EST 04-OCT-2001
60304354F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175684 5',
mRNA sequence.
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1 (bases 1 to 1787)
Nath-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAM1137 row: k column: 13
High quality sequence start:
High quality sequence start:
Location/Qualifiers
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Pred. No. 2.9e-68;
0; Mismatches 33;
333
   301 TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT
                                                                   386 Treegecaegeaceaagereacereaceraeger
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/organism="Homo sapiens"
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Best Local Similarity 90.1%;
Matches 300; Conservative 0
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Homo sapiens
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1 (Dasea I to '76)
Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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/note="Vector: pBluescript sk(-); Site_l: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Pax: 86-21-50801922
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84.1%; Score 280.2; DB 9; Length
Best Local Similarity 90.1%; Pred. No. 2.9e-68;
Matches 300; Conservative 0; Mismatches 33; Indels
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mol_type="mRNA"

/db_xref="taxon:9606"

/clone="GKCGXG07"

tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai
Location/Qualifiers
   TTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 t
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/tissue type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: Xho1;
Site_2: Encel; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/Xho1 sites using the following 5' adaptor: agcAcGAGGG(). Size-selected >500bp for average insert size 1.8kb. Library, constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                    BG197282 112-MAR-2001 RNA linear EST 12-MAR-2001 02439065F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4565272 5',
                                                                                             CAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Context: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1282 row: a column: 17
High quality sequence stop: 840.
Location/Qualifiers
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181 TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleosto
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 840)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                          TTCGGAACTGGGACCAAGGTCACGTCCTAGGT 421
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4565272"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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/lab_host="DH10B (phage-resistant)"
/clone lib="MIH MGC 48"
/clone lib="MIH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIX/XhoI sites using the Directionally cloned into EcoRIX/XhoI sites alsing the following 5' adaptor: GGGAGGGGG, Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the labbratory of Gerald M. Rubin (University of Callifornia, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                       BGS637827F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4765447 5', mRNA sequence.
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                               TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 829)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: capabbs-remail.nth.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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                                                                                                  301 TTCGGAAGAGGACCCGGTTGACCGTCCTAGGT
                                                                                                                                            389 TTCGGCGGAGGACCAAGGTGACCGTCCTAGGT
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/mol_type="mRNA"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 843)
                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
Homo sapiens
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Matches 300; Conservative
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/lab host="DH108 (T1 phage-resistant)"
/clone lib="NHH MGC 77"
/clone lib="NHH MGC 77"
/note="Organ: lung; 'Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggocgctccggc); Site_2: Sfil (ggccattatggc); 57 and
3. adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCGGACATG-TG (3) BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."
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602503383F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4616829 5',
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TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov
Hitgh quality sequence stop: 834.
                                                                                                                                                                                                          181 TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
                                                                                                                                                                                                                                                              241 CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTA
                                                                                                       CACCCAGGCAAAGCCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC
                                                                                                                                                         211 cccccasscacascccccaaacrcatsattatsasstcasstratcsscccrcassgc
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 3.1e-68;
0; Mismatches 33; Indels
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/db_xref="taxon:9606"
/clone="IMAGE:4616829"
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90.1%;
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Matches 300; Conservative
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Best Local Similarity 90.8
Matches 297; Conservative
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                                                   CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTCTGGGTCTCCTGGACAGTCGATCACCTTC 156
                                                                                                         TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120
                                                                                                                                                                                              CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAAGCGGGCCTCAGGGGTC 180
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                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="germinal center B cells"
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/lab_host="MHDB [LT]"
/clone_lib="NHH_MGC_37"
/note=="Vector: piv773-pac; Site_l: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Lou
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Exc. RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CLOR Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbr/image/image.html

Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                   TCTGATCGCTTCTCGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCGGAACTGGGACCAAGGTCACCGTCCTAGGT 429
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db_xref="taxon:9606"
/clone="IMAGE:306093"
/tissue_type="lymph"
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Score 279; DB 9; Length 417;

83.8%;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 GAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTCGGA 306
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                                                                       7 GCCCCGACTCAGCCTCCCTCTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCCTGC
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Job time : 1441.93 secs
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Recombinant human

Mouse DNA encoding Thrombopoietin (TP Mouse DNA encoding Human immune syste Variable region of Human autoantibody Antibody D lambda

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Coding sequence fo Coding sequence fo MH4H7 MAb light ch

throm

DNA encoding

Human anti-Pseudom

DNA encoding anti-DNA encoding a var DNA encoding novel Human U266 lambda

U266-Lambda gene a DNA encoding novel Monoclonal antibod

Monoclonal antibod DNA encoding novel Human autoantibody

Title: Perfect score:

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Anti-human CD23 6G5 monoclonal antibody light chain variable region DNA.
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/product= "anti-human CD23 6G5 light chain variable
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124..165
/*tag= d
/note= "encodes CDR l region"
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                                                           ABK71411
ABK70104
ABX00208
ABX70114
ABX00191
ABX71397
ABX71019
AAX31654
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AAX40317
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AAC67868
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Human autoantibody
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(c) 1993 - 2003 Compugen Ltd.
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Score

Result ŅO.

Human prostate exp Bicistronic idioty DNA encoding anti-DNA encoding novel

EBV transformant a DNA encoding monoc Human prostate exp Human; colon adenocarcinoma; colon cancer; tumour; gene; ss

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King GE,

Meagher MJ,

(CORI-) CORIXA CORP

WPI; 2002-098052/13

07-JUN-2001; 2001WO-US18574. 09-JUN-2000; 2000US-210667P. 22-NOV-2000; 2000US-252614P.

WO200196389-A2.

20-DEC-2001

Colon adenocarcinoma-specific cDNA #264

23-APR-2002

ABK29738;

BP.

ABK29738 standard; cDNA; 605

RESULT 2 ABK29738

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note= "encodes CDR 2 region"
                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Pages 102-104; 146pp; English.
                                       728..357
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Matches 333; Conservative
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05-FEB-1998;
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The invention relates to an isolated polynucleotide (I) encoding a colopypeptide (II) comprising a portion of a colon tumour protein. A new colsymbotide (III) that hybridises to (I) is useful for determining the presence of a cancer in a patient. (II) or antigen presenting calls specific for a tumour protein, by contacting T cells capacific for a tumour protein, by contacting T cells or antigen presenting cells that express (II). (II). (II) or antigen presenting cells that express (II) are useful for treating colon cancer in a patient by incubating CD4 and/or CD8+ T cells isolated from a patient with (I), (II), or antigen presenting cells that express (II), so that T cells proliferate, and administering to the patient and cffective amount of the proliferated T cells, thus inhibiting the cavelopment of a cancer in the patient. A new composition is useful in stimulating an immune response in a patient. (I) or (II) is useful in colon cancer and for the diagnosis and monitoring of the cancers (I), (II) or an antibody against (II) is useful as a probe or primer for or therapy of human colon cancer. (I) is useful as a probe or primer for molecic acid hybridisation, and in the design and preparation of tibozyme colon cancer of the proliferate design and preparation of tibozyme colon cancer of the substitution of (II) in tumour cells ABK29475.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              v isolated polynucleotide encoding a polypeptide comprising a portion colon tumour protein, for detection, diagnosis and therapy of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGTCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGGTCTCCTGGACAGTCGGTCACCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.1%; Score 286.6; DB 24;
llarity 91.3%; Pred. No. 6.9e-80;
Conservative 0; Mismatches 29;
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WPI; 2003-103417/09.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The specification describes a method for the intracellular analysis of a target molecule within a biological cell. The method comprises expressing within the cell a first polypeptide sequence comprised of a first reporter species capable of binding to the target molecule and a first reporter molety attached to the first binding species; expressing within the cell as second polypeptide sequence comprised of a second binding species capable of competing with the target molecule for binding species capable of competing with the target molecule for binding species capable of competing with the target molecule for binding of the first binding of competing with the target molecule for binding of the first binding species and a second reporter moieties binding species the first and second reporter moleties binding a signal that can be differentiated from one capable of being generated when the first and second reporter moieties do not interact; and effecting a measurement to determine the presence capable of being generated when the first and second reporter moieties do not interact; and effecting a measurement to determine the presence or signal representative of binding of the first and second binding species. The method is useful for the intracellular analysis of a target molecule, e.g. for detecting the presence and/or amount of target contractions of intracellular molecules. The present sequence represents interactions of intracellular molecules. The present sequence represents a plasmid used in an intracellular assay for the MUCI epitope of human mucinl, demonstrating the method of the invention. In this assay,
                                           240
TCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGCGCCTCCCTGACCATCTCTGGGCCTC 329
                                                                                                 CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTA 300
                                                                                                                           CAGGCTGAGGACGAGGCTGATTATTACTGCAGCTCATATACTAGCATCATCACTGTGGTA 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Intracellularly analysing or detecting the presence of a target molecule within a biological cell, by determining the presence or signal representative of binding of polypeptide species to the target
                                                                                                                                                                                                                                                                                                                                                                 Intracellular analysis; intracellular interaction; intrabody; ScFv; MUC1; mucin 1; pScFv-ECFP2; ss.
                                                                                                                                                                        TTCGGCGGAGGACCAAGGTGACCGTCCTAGGT 422
                                                                                                                                                       TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 333
                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence of plasmid pScFv-ECFP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example; Page 29-31; 51pp; English
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                                                                                                                                                                                                                                                       ABV77130 standard; DNA; 5464 BP
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                                                                                                                                                                                                                                                                                     9
the first polypeptide is an anti-MUC1 ScFv, and the second polypeptide comprises the MUC1 epitope attached to yellow fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                                                          TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
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0
                                                                                                                                                  Score 284; DB 25; Length 5464;
Pred. No. 1e-78;
0; Mismatches 30; Indels 0
                                                                                        Sequence 5464 BP; 1294 A; 1485 C; 1468 G; 1217 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence of plasmid pBudMUC-EYFPscFvECFP.
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                                                                                                                                                      / Match 85.3%;
Local Similarity 91.0%;
les 302; Conservative C
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moiety attached to the first binding species; expressing within the cell
moiety attached to the first binding species; expressing within the cell
capable of competing with the target molecule for binding species
capable of competing with the target molecule for binding species
competing with the target molecule for binding species capable
cof competing with the target molecule for binding species capable
cof competing with the target molecule for binding species
cof species and a second reporter moiety, the first and second reporter
moieties being such that on binding together of the first binding
be capable of producing a signal that can be differentiated from one
capable of baing generated when the first and second reporter moieties
con interact; and effecting a measurement to determine the presence
cor signal representative of binding of the first and second binding
concluse; The method is useful for the intracellular analysis of a target
molecules in cells. The method is also useful for studying the
conclusions of intracellular molecules. The present sequence represents
content in the mointracellular assay for the MUCI epitope of
chuman mucini, demonstrating the method of the invention. In this assay,
the first polypeptide is an anti-wood computation protein.
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85.3%; Score 284; DB 25; Length 6877;
Best Local Similarity 91.0%; Pred. No. 1.1e-78;
Matches 302; Conservative 0; Mismatches 30; Indels 0;
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181 TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGGCTC 240
                                                         CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTGTTA 300
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APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta; dermatological; immunosuppressive; antiinflammatory; antiinhumatic; antiarthritic; cytostatic; antiamemic; antiallergic; antiathmatic; neuroprotective; ophthalmological; tuberculostatic; antidiabetic; antipsoriatic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic; inflammatory disorder; proliferative disorder; single chain antibody; antibody; gene; se.
4605 TTCGGCGGAGGGACCAAGGTCACCGTTCTAGG 4636
                                                                                                                                                                                                                   APRIL binding scFv A027A11 encoding DNA.
                                                                                              ABZ25504 standard; DNA; 726
                                                                                                                                                                              (first entry)
                                                                                                                                                                              28-MAR-2003
                                                                                                                                       ABZ25504;
                                                       RESULT 5
                                                                             ABZ25504
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GVHD;

Synthetic

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The invention relates to a novel antibody or its fragment, which immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL). The antibody of the invention has dermaclogical, immunosuppressive, antiantabedy of the invention has dermaclogical, immunosuppressive, antialtametory, antitheumatic, antiarthritic cytostatic, antianamic, antialta, ant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated antibody that immunospecifically binds tumor necrosis factor delta, useful for treating, preventing or ameliozating Onn-Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.1%; Score 283.4; DB 25; Length
90.7%; Pred. No. 7.5e-79;
tive 0; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 726 BP; 156 A; 199 C; 220 G; 151 T; 0 other;
                                                                       /product= "A027All scFv"
/note= "No start/stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Page 192; 225pp; English
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunospecifically bind to APRIL.
                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                   22-MAY-2002; 2002WO-US16106.
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P-PSDB; ABP60522.
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fragment. The fragment is used to produce a mixture or panel of 5
different specific binding members, each comprising an antibody VH
and/or VL variable domain and capable, when displayed on the surface
of filamentous bacteriophage particles or in the case of a specific
binding member comprising the DS VH and/or VL variable domain when
bound to human serum amyloid protein, to pass through a mammalian
blood brain barrier (BBB). The panel is useful for the selection of
specific binding members with a desired property such as ability to bind endothelial cells or other brain cell antigen,
ability to bind areas of inflammation in the brain or BBB breakdown or
ability to bind intracellular adhesion molecules and to bind transferrin
receptor. The antibodies are useful in diagnosis, prophylaxis and
treatment of human or animal body, including neurological diseases, such
CAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTGTTA 300
                                                                                                                                       endothelial čell; brain cell antigen; inflammation; adhesion molecule;
transferrin receptor; neurological disease; Alzheimer's disease;
prion disease; AIDS-related dementia; epilepsy; brain injury; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody; light chain; VL; amyloid protein; blood brain barrier;
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                                                                                                                                                                                                                            TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 333
                                                                                                                                                                                                                                                                    TTCGGCGGAGGACCAAGCTGACCGTCCTAGGT
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P-PSDB; AAG62957.
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                                                                                                                                                                                                                                                 TCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACAATCTCTGGGCTC
                                                                         TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of variable light chain fragment of clone G102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chain; VL; amyloid protein; blood brain barrier;
                                                                                                                                                                                                                                                                                                                                                                                                     TTCGGCGGGGGGCCAACCGTCCTAGG 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cross BBB, ability to bind endothelial cells or other brain cell antigen, ability to bind areas of inflammation in the brain or BBB breakdown or ability to bind intracellular adhesion molecules and to bind transferrin receptor. The antibodies are useful in diagnosis, prophylaxis and treatment of human or animal body, including neurological diseases, such as Alzarienter's disease, prion disease, NISS-related dementia, epilepsy and traumatic brain injury and any diseases involving inflammation occurring within the brain or central nervous system.
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                                                                                                                                                                                                                                                                                                                                                                                                                  TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
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0
                                                                                                                                                                  DB 22; Length 333;
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                                                                                                                                                               84.3%; Score 280.8; DB 22;
90.4%; Pred. No. 3.7e-78;
ive 0; Mismatches 32;
                                                                                                                                     Sequence 333 BP; 72 A; 99 C; 86 G; 76 T; 0 other;
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                                                                                                                                                                              larity 90.4%;
Conservative
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P-PSDB; AAG80206.
                                                                                                                                                               Query Match
Best Local Similarity
Matches 300; Conserv
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This invention describes a novel fusion protein (I) that has, at its N-terminus, one or more epitopes that bind specifically to autoantibodies (AAb) against the islet cell antigen IA2 and, at its C-terminus, one or more epitopes that bind specifically to antibodies (Ab) directed against the glutamate decarboxylase GAD65. (I), also nucleic acid (II) encoding the year containing (II) and transformed cells, are useful for diagnosis and prognosis of diabetes mellitus type 1, stiff-man syndrome, polyglandular autoimmune syndrome or other autoimmune conditions of diagnosis of high specificity and sensitivity, capable of recognizing antibodies against both IA2 and GAD65, simultaneously. Unlike known tusions, where the GAD65 component is at the N-terminus, (II) contains correctly folded conformational epitopes that can react with most MICA autoantibodies. This sequence encodes the human autoantibody MICA-I variable region heavy chain used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cgaggcrgarrarracrgcagcrcararacaagcagcagcagcacrcrggrarrcggcggagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; antibody scFv; TN11; Tenascin-C; TN-C; domain C-containing TNC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACTICAGCCTGCCTGCTGTGTGTGTGTGGACAGTCGATCACCATCTCCTGCACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 AACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCACCCAGGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
metabolic diseases, is reactive with autoantibodies against both glutamate decarboxylase and islet cell antigen
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                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                   Seguence 351 BP; 71 A; 106 C; 91 G; 83 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                                                                                                                                                                                               / Match 84.2%; Score 280.4; DB Local Similarity 91.9%; Pred. No. 5e-78; nes 296; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCFv TN11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312 GACCCGGTTGACCGTCCTAGGT 333
                                                                    Disclosure; Page 22; 68pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC67868 standard; DNA; 747
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches
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The present sequence encodes a recombinant human antibody scFv. Antibody TN11 reacts with the long form of human Tenascin-C (TN-C). The epitope recognised by TN11 is located inside domain C of TN-C. TN11 is therefore only capable of recognising TN-C isoforms containing domain C (CTN-C). TN11 is useful for detecting the presence of TN-C isoforms in vitro or in vivo for diagnosing pathologies expressing the cTN-C isoforms of TN-C. It is useful for the preparation of formulations for the treatment of
                                                                                                                                                                                                   ō
                                                                                                                                                                                Ligands used for diagnosis and treatment of human neoplasias, are capable of identifying the tenascin-C isoform containing domain C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21; Length 747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 747 BP; 157 A; 197 C; 231 G; 162 T; 0 other;
                                                                                                                                                                                                                                                       Claim 8; Page 5-6; 31pp; English
                 99IT-FI00094
                                                   (PHIL-) PHILOGEN SRL
                                                                                                                        WPI; 2000-687225/67.
                                                                                                                                                                                                                                                                                                                                                                                                                            human neoplasias.
                                                                                                                                             P-PSDB; AAB36083
                 20-APR-1999;
                                                                                                                                                                                                                      tenascin-C -
                                                                                        Zardi
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Novel modified virus comprising non-native polypeptides with stable conformation and having framework moieties containing binding moieties which confer upon the virus, an altered tropism, useful in gene therapy

Boulanger PA;

Lindholm L, Nord AK, WPI; 2002-217049/27

GOT-A-GENE AB

(GOTA-) (GARD/)

19-JUL-2001; 2001WO-GB03252. 19-JUL-2000; 2000GB-0017720

NO200208263-A2 31-JAN-2002 Example 10; Page 148; 163pp; English

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The invention describes a modified virus comprising non-native polypeptides which has framework moieties each containing binding polypeptides which has altered tropism conferrad by the binding moieties, where the virus has altered tropism and nucleus of mammalian host cell in conformation which is maintained in absence of ligands for the binding moieties, where the conformation allows the binding moiety subsequently to bind with the ligand. The modified virus is useful in therapy for the preparation of a medicament for treating tumnour cells, cancer, proliferating cells, vascular diseases.

Inflammatory diseases and infectious diseases such as Human immunodeficiency virus (HIV). The altered tropisms allow the virus to be used in treatment of disease in human or animal subjects, either by in vivo treatment of, or ex vivo treatment of cells of, the subject requiring treatment. The problems associated with the expression of functional non-native viral components in the nucleus and cytosol of host cells is solved by using the modified virus for the purpose. This fragment (FV) used in the creation of the modified virus containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           non-native polypeptides.
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Pred. No. 7.7e-78;
0; Mismatches 33; Indels
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Sequence 816 BP; 181 A; 220 C; 238 G; 177 T; 0 other;
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                                                                                                                                                                       Score 280.2; D
Pred. No. 8e-78
0; Mismatches
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90.1%;
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715

disease;

DNA encoding anti beta-galactosidase single chain Fv fragment

(first entry)

05-JUN-2002

ABK43226;

ABK43226 standard; DNA; 816

RESULT 10 ABK43226

Modified virus; cytostatic; gene therapy; tumour cell; trocoliferating cell; cancer; vascular disease; inflammatory infectious disease; human immunodeficiency virus; HIV; immunoglobulin; beta-galactosidase; variable fragment; Fv;

Unidentified

gene;

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CACCCAGGCAAAGCCCCCAAACTCATCATTATGAGGTCAGTAATCGGCCCTCAGGGGTT 235
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                                                                                                                                                                                                                     ABX00205 standard; DNA; 792
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17-APR-2001; 2001WO-JP03288.
12-SEP-2001; 2001JP-0277314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-OCT-2001; 2001WO-JP09260.
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2000JP-0321822.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHUS ) CHUGAI SEIYAKU KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tsuchiya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-682599/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorders and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; ABG97834.
                                                                                                                                                                                                                                                                                                                                                                                                             WO200233073-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-OCT-2000;
20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fukushima N,
                                                                                                                                                                                                                                                                                                                                                                                                                                      25-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                              ABX00205;
   176
                            181
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                                                                                                                                                                                            RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a new isolated nucleic acid termed ovarian specific nucleic acid (OSNA) comprising: (a) a nucleic acid molecule that encodes any of 53 fully defined protein sequences appearing as ABUG1018-ABUG1070 (termed ovarian specific proteins, OSP); (b) any of 76 fully defined nucleotide sequences appearing as ABX92187-ABX92262; or (c) a sequence having at least 60% sequence identity to the nucleic acid molecule of (a) or (b). Also included are a method for determining the presence of an ovary specific nucleic acid (OSNA) in a sample, a vector comprising an OSNA, a host cell comprising the vector, an isolated OSP polypeptic an anti-OSP antibody or fragment, an enthod for determining the presence of an ovary specific protein in a sample and a vaccine comprising an OSP or OSNA. The methods and compositions of the present invention are useful for identifying.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGTCTGCCCTGACTCAGTCTGCCTCCGTGTCTCGGGTCTCCTGGACAGTCGCATCATC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 recrecacregaaccageagreaceregregregrearerarererecregraceadag 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACCCAGGAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CAGTCTGCCCCGACTCAGCCTCCCTCTGTGTCTCCTGGGTCTCCTGGACAGTCGGTCACCATC
                                                                                                                                          Human, gene, 88; ovarian specific nucleic acid; OSNA; ovarian cancer; non-cancerous ovarian disease; gene therapy; vaccine; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated OSNA nucleic acid and encoded polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating ovarian cancer and non-cancerous diseases in ovarian tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosing, monitoring, staging, imaging and treating ovarian can
non-cancerous disease in ovary tissue. The present sequence is an
                                                                                                                                                                                                                                                                                                                                                             Cafferkey R;
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~hes 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1460 BP; 351 A; 466 C; 401 G; 241 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                             Karra K,
                                                                                                                   Human ovarian specific nucleic acid DEX0310 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.2%; Scc. No. 1c. 89.5%; Pred. No. 1c. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                             Recipon H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 146; 224pp; English.
                                           ABX92194 standard; cDNA; 1460 BP.
                                                                                                                                                                                                                                                                                                                                                               Hu P,
                                                                                                                                                                                                                                                                         13-FEB-2002; 2002WO-US22271.
                                                                                                                                                                                                                                                                                               13-FEB-2001; 2001US-268290P.
15-FEB-2001; 2001US-268834P.
                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 89.5
Matches 298; Conservative
                                                                                                                                                                                                                                                                                                                                                               Macina RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the invention.
                                                                                                                                                                                                                                                                                                                                    (DIAD-) DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-120677/11.
                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; ABU61023
                                                                                                                                                                      gynaecological
                                                                                                                                                                                                                       WO200292785-A2
                                                                                                                                                                                                                                                                                                                                                                          Liu C;
                                                                                                                                                                                               Homo sapiens
                                                                                            08-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                Ś
                                                                    ABX92194;
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                                                                                                                                                                                                                                                                                                                                                             Salceda
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                                                                                                                                                                                                                                                                                                                                                                          Sun X,
                               ABX92194
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The invention relates to a new modified single chain Fv antibody
containing at least two Heavy chain variable domains and at least two
light chain variable domains from the same or different monoclonal
antibodies and which is an agonie for crosslinking a molecule at the
cell surface or within the cell and thereby transducing a signal into the
cell. Also include are the DNA encoding the antibody, animal cells and
microorganisms transformed by and expressing the DNA; the preparation of
the antibodies by culture of the transformed cells, drug compositions
containing the antibodies and an assay method for the agonist activity
of the antibodies by contacting the antibodies with cells expressing the
relevant cell surface or internal molecule. The antibodies are useful for
treatment and prevention of cancer, inflammatcry disease, hormonal
disorders including diabetes, autoimmune disease, leukaemia,
disordering an antibody of the invention or a fragment thereof.
                                                                             295
                                                                                                                                                                    241 CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTA 300
                                                                                                                                                                                                                      ds; gene; monoclonal antibody; signal transduction agonist; cancer; inflammatory disease; dysendocrinism; blood disease; leukaemia; cytostatic; antiinflammatory; immunosuppressive; immunostimulant;
TCTGATGGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
                                                                                  renalicierrenegenceaerenegealenegeereereereereereere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ë
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hormonal disorder; diabetes; autoimmune disease
                                                                                                                                                                                                                                                                                                                                                      333
                                                                                                                                                                                                                                                                                                                                                                                                                                         rreggacregaceasereacerectaser 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohtomo T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding single chain antibody 12E10 Fv.
                                                                                                                                                                                                                                                                                                                                                           TTCGGAAGAGGACCCGGTTGACCGTCCTAGGT
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GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTC 303
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                    antibody, and exhibits thrombopoietin (TPO) agonistic effect by causing the TPO receptor to crosslink. The antibodies are useful in preventives and/or remedies for platelet reduction-associated blood diseases, thrombocytopenia following cancer chemotherapy or leukaemia. The antibody can act as a TPO signal transduction agonist by transducing a signal into cells by crosslinking a TPO receptor to exert TPO agonism. This sequence encodes a thrombopoietin (TPO) agonist antibody associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               608 AATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT
chain variable domains and 2 or more light chain variable domains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ds; gene; monoclonal antibody; signal transduction agonist; cancer; inflammatory disease; dysendocrinism; blood disease; leuke cytostatic; antiinflammatory; immunosuppressive; immunostimulant; hormonal disorder; disebetes; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                         DB 24; Length 792;
                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                               C; 217 G; 174 T; 0 other;
                                                                                                                                                                                                                                                                                                                                   Score 276.8; DB 24;
Pred. No. 9.2e-77;
0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding single chain antibody sc12E10 Fv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331
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2001WO-JP01912.
2001WO-JP03288.
2001JP-0277314.
                                                                                                                                                                                                                                                                                                                                   83.1%;
llarity 90.2%;
Conservative
                                                                                                                                                                                                                                                                                  Sequence 792 BP; 170 A; 231
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                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 296; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-OCT-2000;
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12-MAR-2001;
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                                                                                                                                                                                                                                                                                  TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC 123
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                                                                                                                                                                                                                                                                                                                                                                                                183
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                                                                                                                                                                          CACCATCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified antibody; thrombopoietin; TPO; agonist;
TPO receptor; platelet reduction-associated blood disease;
thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction;
                                                                                                                      Gaps
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                                                         DB 24; Length 792;
                                                                                                                                                                       4 TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGG1
                                                                                                                Indels
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     C; 217 G; 174 T; 0 other;
                                                      Score 276.8; DB 24;
Pred. No. 9.2e-77;
0; Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
                                                         83.1%;
llarity 90.2%;
Conservative
  A; 231
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12-SEP-2001; 2001JP-0277314
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     BP; 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohtomo
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296; Conserv
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                                                            Query Match
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leukaemia;

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Degraded thrombopoietin agonist antibodies containing H and L chain V domains of monoclonal antibody, useful in preventives and/or remedies for blood diseases, thrombocytopenia following cancer chemotherapy or
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17-APR-2001; 2001WO-JP03288.
12-SEP-2001; 2001JP-0277314.
                                                                                                                             22-OCT-2001; 2001WO-JP09259
                                                                                                                                                                                                                                                                              (CHUS ) CHUGAI SEIYAKU KK
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                                                                                                                                                                                                                                                  The invention relates to a new modified single chain Fv antibody containing at least two Heavy chain variable domains and at least two Light chain variable domains and at least two Light chain variable domains from the same or different monoclonal antibodies and which is an agonist for crosslinking a molecule at the cell surface or within the cell and thereby transducing a signal into the cell surface or within the cell and thereby transducing a signal into the cell surface or within the cell and expressing the publy, animal cells and microorganisms transformed by and expressing the preparation of the antibodies by culture of the transformed cells, drug compositions containing the antibodies by contacting the antibodies with cells expressing the relevant cell surface or internal molecule. The antibodies are useful for treatment and prevention of cancer, inflammatory disease, hormonal disorders including diabetes autoimmune disease, leukaemia dysendocrinism and blood disorders. The present sequence is a DNA sequence encoding an antibody of the invention or a fragment thereof.
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                                                                                                    Modified single chain multimeric Fv antibody acting as a signal transduction agonist for treatment of inflammatory hormonal and blood
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90.2%; Pred. No. 9.3e-77;
ive 0; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 822 BP; 169 A; 233 C; 235 G; 185 T; 0 other;
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Matches 296; Conservative
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                        WPI; 2002-682599/73.
P-PSDB; ABG97835.
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                                                The invention describes a modified antibody comprising at least 2 heavy chain variable domains and 2 or more light chain variable domains of an antibody, and exhibits thrombopoletin (TPO) agonistic effect by causing the TPO receptor to crosslink. The antibodies are useful in preventives and/or remedies for platelet reduction-associated blood diseases, thrombocytopenia following cancer chemotherapy or leukaemia. The antibody can act as a TPO signal transduction agonist by transducing a signal into cells by crosslinking a TPO receptor to exert TPO agonism. This sequence encodes a thrombopoietin (TPO) agonist antibody associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 822 BP; 169 A; 233 C; 235 G; 185 T; 0 other;
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Example 8; Page 208-209; 213pp; Japanese.
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completed: December 29, 2003, 16:25:34 me : 146.29 secs

time Search Job tim

Modified antibody; thrombopoietin; TPO; agonist; TPO receptor; platelet reduction-associated blood disease; thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction;

Synthetic

gene; ds

Sequence

Sequence 970,

Sequence

15053,

Sequence 63, Sequence 18, Sequence 150

Sequence 6 Sequence 6 Sequence 1

Sequence Sequence Sequence

18093

Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence

Perfect score:

Sequence:

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OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB 8 Maximum DB 8

Database

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TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE THEREOF AS THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS,
STREET: P.O. BOX 1404
US-10-039-785-54
US-09-974-449-7
US-10-139-748-7
US-10-139-748-60
US-10-139-785-60
US-10-139-785-60
US-10-139-785-60
US-10-139-785-16500
US-10-188-846-13540
US-10-188-846-13540
US-10-122-673-63
US-10-022-386-1351
US-10-022-386-1351
US-10-022-386-1351
US-10-022-188-13
US-10-022-188-13
US-10-139-785-61
US-10-139-785-61
US-10-139-785-61
US-10-139-785-61
US-10-139-785-55
US-10-039-785-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,441
FILING DATE: 05-Feb-1998
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09019441
Publication No. US20030086921A1
GENERAL INFORMATION:
APPLICANT: REFF. Mitchell E.
KLOETZER, William S.
NAKAWURA, Takehiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                    78.6
4.87
78.4
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78.4
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                                                                                                                                             December 29, 2003, 19:01:43; Search time 481.099 Seconds (without alignments) 2371.523 Million cell updates/sec
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1 CAGTCTGCCCCGACTCAGCC......CCCGGTTGACCGTCCTAGGT 333
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Sequence 5
Sequence 5
Sequence 6
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Sequence 8
Sequence 3
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1: /cgn2_6/ptodate/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodate/2/pubpna/PCT_MEW_PUB.seq:*
3: /cgn2_6/ptodate/2/pubpna/PCT_MEW_PUB.seq:*
4: /cgn2_6/ptodate/2/pubpna/US06_NEW_PUB.seq:*
5: /cgn2_6/ptodate/2/pubpna/US06_NEW_PUB.seq:*
6: /cgn2_6/ptodate/2/pubpna/US08_NEW_PUB.seq:*
7: /cgn2_6/ptodate/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodate/2/pubpna/US08_PUBCOMB.seq:*
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12: /cgn2_6/ptodate/2/pubpna/US10A_PUBCOMB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:
                           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-019-441-1

US-10-10-686-1

US-10-151-882-4

US-10-139-785-63

US-10-139-785-64

US-10-139-785-64

US-10-039-785-64

US-10-039-785-64

US-10-039-785-64

US-10-039-785-64

US-10-198-846-13540

US-10-198-846-13540

US-10-198-846-13206

US-10-139-846-13206

US-10-139-846-13206
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                                                                                                                                                                                                                                                                                                                                                                           2244575 segs, 1713117285 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                             sw model
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                                                                                                                                                                                                                                                                                                                              Gapop 10.0 , Gapext 1.0
                                                                                                           nucleic search, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq length: 0
seq length: 200000000
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1640
735
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Match ]
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2883.4 2883.4 2283.4 2283.4 2283.4 200.2 2

Score

Result Š.

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61 TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTA 300
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Publication No. US20030059862A1
GENERAL INFORMATION:
APPLICAUT: Ruben, Steven M.
TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
FILE REPRESENCE: PP554
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR PILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SSOFTWARE: Patentin version 3.0
SSOTUM APPLICATION NUMBER: US/10/151,882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 TCTGATCGCTTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 333; DB 15;
100.0%; Pred. No. 7.2e-102;
tive 0; Mismatches 0;
           ATTORNEY AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTATION UNBER: 35,030
REFERENCE/DOCKET WUMBER: 012712-353
TELECOMMUNICATION INFORMATION:
TELEFRANCE (703) 836-620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 TTCGGAAGAGGACCCGGTTGACCGTCCTAGGT 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: DNA encoding A027All scFv
                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 58.7390
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                    1..390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 333; Conservative
                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                              FEATURE
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US-10-151-882-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 TCCTGCACTGGAACCAGCGATGACGTTGGTGTTATAACTATGTCTCCTGGTACCAACAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 CAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTA 300
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                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Publication No. US20030059424A1
GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
KLOETZER, William S.
NAKAMURA, TAKehiko
TITLE OF INVENTION: GAMMA, TAKEHOUSE AND USE THEREOF AS THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                              Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: BOX 1404
CITY: Alexandria
CITY: Alexandria
COUNTR: Virginia
COUNTR: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBP C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/103,686
FILING DATE: ZS-Mar-2002
CLASSIFICATION: ADMARA:
APPLICATION NUMBER: US/10/103,686
FILING DATA:
APPLICATION NUMBER: US/10/103,686
FILING DATA:
APPLICATION NUMBER: US/10/103,686
FILING DATA:
APPLICATION NUMBER: US/10/103,686
                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 333; DB 11; Best Local Similarity 100.0%; Pred. No. 7.2e-102; Matches 333; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCGGAAGAGGACCCGGTTGACCGTCCTAGGT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 TTCGGAAGAGGACCCGGTTGACCGTCCTAGGT 333
                                                                                                                                                                                                                                        LOCATION: 58. 390
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                  NAME/KEY: mat_peptide
                    LENGTH: 390 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           1..390
                                                                                                                                                                           LOCATION:
                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                   US-09-019-441-1
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US-10-103-686-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 63, Application US/10139785
Publication No. US20030190685A1
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Matches 302; Conservative
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APPLICANT: Salcedo et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Receptors

FILE REFERENCE: PF550

CURRENT APPLICATION NUMBER: US/10/139,785

CURRENT FILING DATE: 2002-05-07

PRIOR APPLICATION NUMBER: 60/341,237

PRIOR FILING DATE: 2001-12-20

PRIOR APPLICATION NUMBER: 60/341,337

PRIOR FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-11-09

PRIOR FILING DATE: 2001-11-09

PRIOR FILING DATE: 2001-11-09

PRIOR FILING DATE: 2001-09-21

PRIOR FILING DATE: 2001-09-21

PRIOR FILING DATE: 2001-09-21

PRIOR FILING DATE: 2001-09-21

PRIOR FILING DATE: 2001-06-04

PRIOR FILING DATE: 2001-06-05

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                                                                          Score 283.4; DB 15; Length
Pred. No. 4.7e-85;
0; Mismatches 31; Indels
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US-10-139-785-59
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Publication No. US20030190685A1
                                                                               85.1%;
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ORGANISM: Artificial sequence
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LENGTH: 73
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Matches 302
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GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REPERENCE: PF56
CURRENT APPLICATION NUMBER: US/10/139,785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR PILING DATE: 2001-12-20
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-22
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-22
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-22
PRIOR FILING DATE: 2001-09-23
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 66
SEQ ID NO 63
LEMCTH: 735
LEMCTH: 735
LEMCTH: 735
TCCTGCACTGGAACCAGCGATGACGTTGGTGATAACTATGTCTCCTGGTACCAACAC
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CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
PRIOR FILING DATE: 2001-12-20
PRIOR FILING DATE: 2001-12-20
PRIOR FILING DATE: 2001-11-4
PRIOR FILING DATE: 2001-11-4
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/329,176
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-04
PRIOR FILING DATE: 2001-08-05
PRIOR FILING DATE: 2001-08-05
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-06-05
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Best Local Similarity 90.77
Matches 302; Conservative
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SOFTWARE: Patentin Ver. 2
SEQ ID NO 59
LENGTH: 735
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APPLICANT: Salcedo et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

CURRENT APPLICATION NUMBER: US/10/139,785

CURRENT FILING DATE: 2002-05-07

PRIOR FILING DATE: 2002-04-05

PRIOR APPLICATION NUMBER: 60/331,310

PRIOR APPLICATION NUMBER: 60/331,310

PRIOR PRIOR DATE: 2001-11-14

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-10-09

PRIOR FILING DATE: 2001-00-09

PRIOR FILING DATE: 2001-09-21

PRIOR FILING DATE: 2001-09-21

PRIOR PRIOR PRIOR DATE: 2001-09-21

PRIOR PRIOR APPLICATION NUMBER: 60/309,176

PRIOR PRIOR DATE: 2001-09-21

PRIOR FILING DATE: 2001-09-21

PRIOR FILING DATE: 2001-06-04

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-04

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-06-04

PRIOR FILING DATE: 2001-06-05-25

NUMBER: PACENTALE, PACENTIN VOIL 06-25
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US-10-139-785-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-139-785-64
; Sequence 64, Application US/10139785
; Publication No. US20030190685A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial sequence
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JAPPLICANT: Salcedo et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Receptors

TITLE OF INVENTION: Receptors

TITLE REFERENCE: PF550

CURRENT APPLICATION NUMBER: US/10/039,785

CURRENT FILING DATE: 2002-05-07

PRIOR FILING DATE: 2002-04-05

PRIOR FILING DATE: 2001-12-20

PRIOR FILING DATE: 2001-11-20

PRIOR FILING DATE: 2001-11-13

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-10-09

PRIOR FILING DATE: 2001-10-09

PRIOR FILING DATE: 2001-09-21

PRIOR FILING DATE: 2001-09-21

PRIOR FILING DATE: 2001-09-21

PRIOR FILING DATE: 2001-09-21
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85.1%; Score 283.4; DB 14; Length 735;
Best Local Similarity 90.7%; Pred. No. 4.7e-85;
Matches 302; Conservative 0; Mismatches 31; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCGGAAGAGCCCGGTTGACCGTCCTAGGT 333
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, OTHER INFORMATION: DNA encoding T1015E01 scFv
US-10-039-785-64
                                                                 703 TTCGGCGGAGGACCAGGTCACGTCTAGGT
                               TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PATENTIN VEY: 2.1
                                                                                                                                                                                                                                                         Sequence 64, Application US/10039785
Publication No. US20020067646A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial sequence
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583 TCTAATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 642
                                                                 241 CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTA 300
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APPLICANT: Salcedo et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT APPLICATION NUMBER: G0/369,860
PRIOR FILING DATE: 2002-04-05
PRIOR FILING DATE: 2002-04-05
PRIOR FILING DATE: 2001-12-20
PRIOR FILING DATE: 2001-11-14
PRIOR PAPLICATION NUMBER: G0/331,310
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-0-09-21
PRIOR PLICATION NUMBER: G0/323,807
PRIOR FILING DATE: 2001-06-04
PRIOR PLICATION NUMBER: G0/323,9176
PRIOR FILING DATE: 2001-06-04
PRIOR PLICATION NUMBER: G0/309,176
PRIOR PLICATION NUMBER: G0/294,981
PRIOR PLICATION NUMBER: G0/293,473
PRIOR PLI
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                                                                                                                                                                                                                                                            703 rrcdgcgcgcgcgccaaccrcaccrccracgr 735
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; OTHER INFORMATION: DNA encoding T1015A07 scFv
US-10-039-785-63
                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 63, Application US/10039785; Publication No. US20020067646A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial sequence
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                                                                                                                                                                                                                                                                                                                                                                  Length 1460;
                                                                                                                                                                                                                                                                                                                                                                                                                  35; Indels
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GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBT TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES; FILE REFERENCE: 20411-756; CURRENT APPLICATION NUMBER: US/09/235,076; PRIOR APPLICATION NUMBER: US/09/235,076; PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                  83.2%; Score 277; DB 13;
89.5%; Pred. No. 8.8e-83;
tive 0; Mismatches 35;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 36573
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION UNMBER: 60/268,834
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patentin version 3.1
SEQ ID NO ELENGTH: 1460
                                                                                                                                                                                                                                            NAME/KEY: misc_feature
| LOCATION: (1022) .. (1022)
| OTHER INFORMATION: a, c, g or
US-10-076-747-8
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 89.59
Matches 298; Conservative
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Best Local Similarity 89.2
Matches 297; Conservative
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US-09-918-995-36573
                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapien
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; Publication No. US20030180726A1
; Publication No. US20030180726A1
; GENERAL INPORMATION:
    APPLICANT: Salceda, Susana
; APPLICANT: Hu, Ping
APPLICANT: Recipon, Hu, Peng
APPLICANT: Recipon, Hu, Peng
APPLICANT: Cafferkey, Robert
APPLICANT: San, Yangania
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Ovarian Specific Genes and Fries Reference: Dex. 0315
; CURRENT APPLICATION NUMBER: US/10/076,747
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 60/268,290
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                                                                      Sequence 13540, Application US/10198846

PUDIcation No. US20030099974A1

GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Mang, Yourden
APPLICANT: Wang, Yourden
APPLICANT: Wang, Yourden
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: UNMER: 2002-07-18
CURRENT PILING DATE: 2002-07-18
PRIOR PILING DATE: 2001-07-18
PRIOR PILING DATE: 2001-07-18
PRIOR PILING DATE: 2001-07-18
SOFTWARE OF SEQ ID NOS: 14084
SOFTWARE FEALESC for Mindows Version 4.0
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Pred. No. 7.6e-84;
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90.1%;
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Best Local Similarity 90.1
Matches 300; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
CORGANISM: Homo sapiens
US-10-198-846-13540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 13540
LENGTH: 1597
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Sequence 13206, Application US/10198846
Publication No. US20030099974A1
                 Publication No. US200
GENERAL INFORMATION:
APPLICANT: Lillie, 1
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US-10-198-846-13206
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                      TCTGATCGCTTCTCTGGCTCCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 240
 TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120
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                                                                                                                                                                                                                                     CAGGCTGAGGACGAGGCTCATTATTACAGTTCATATACAACCAGAAGCACTCTCGTC 375
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                                                                  CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC
                                                                                    CACCCAGGCAAAGCCCCCAAACTCATAATTTATGAGGTCAGTAATCGGCCCTCAGGGGTT
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 16692, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
APPLICANT: Hyseq. Inc.
; TITLE OF INVENTION: RROM VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: RROM VARIOUS CDNA LIBRARIES
; TITLE OF INVENTION: RROM VARIOUS CDNA LIBRARIES
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR PLLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16692
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Pred. No. 1.9e-82;
0; Mismatches 36; Indels
                                                                                                                                                                                                                                                                      TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 333
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89.2%;
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Best Local Similarity 89.2
Matches 297; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                          US-09-918-995-16692
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US-09-918-995-16692
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RESULT 14 US-10-198-846-13206/c

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1452 TCCTGCACTGGAACCAGCAGTGATGTTGGTGCTTATAACTTTGTCTCCTGGTACCAACAA 1393
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Fublication No. US20030190685A1

GENERAL INFORMATION:
APPLICANT SAlcade et al.
TITLE OF INVENTION: Receptors
TITLE OF INVENTION NUMBER: US/10/139,785

FILE REFERENCE: PFS50

CURRENT APPLICATION NUMBER: US/10/139,785

CURRENT FILING DATE: 2002-05-07

PRIOR PILING DATE: 2002-04-05

PRIOR PILING DATE: 2001-11-2-20

PRIOR APPLICATION NUMBER: 60/341,237

PRIOR APPLICATION NUMBER: 60/341,237

PRIOR APPLICATION NUMBER: 60/341,237

PRIOR PILING DATE: 2001-11-14

PRIOR PILING DATE: 2001-11-14

PRIOR PILING DATE: 2001-11-14

PRIOR PILING DATE: 2001-11-07

PRIOR PILING DATE: 2001-11-07

PRIOR APPLICATION NUMBER: 60/327,364

PRIOR FILING DATE: 2001-11-07

PRIOR PILING DATE: 2001-11-07
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                                                                                                                      AND METHODS
PREVENTION, AND
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APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: VOYEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: POR IDENTIFICATION, ASSESSMENT, PRE;
ITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: RMI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR PILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 1640
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181 TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 240
583 CCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGGCTC 642
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82.2%; Score 273.8; DB 13; Length 735;
Best Local Similarity 88.9%; Pred. No. 8.2e-82;
Matches 296; Conservative 0; Mismatches 37; Indels 0;
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                                                                                                                                                                                                                                                                    TYPE: DNA CRANTSM: Artificial sequence FEATURE: PRATURE: NOTER INFORMATION: DNA encoding T1014A04 scFv US-10-139-785-54
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PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR PELLING DATE: 2001-09-01
PRIOR PILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR PELLING DATE: 2001-06-04
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PALENTIN VEY: 2.1
SEQ ID NO 54
LENGTH: 735
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Sequence 9, Appli Sequence 4, Appli Sequence 133, App Sequence 132, App Sequence 13, Appl Sequence 1, Appli Sequence 3, Appl Sequence 62, Appl

Sequence Sequence Sequence

Sequence Sequence Sequence 1

Sequence

Run on:

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Sequence 1, Application US/08803085;
Patent No. 601138
GENERALI INFORMATION:
APPLICANT: REFF, Witchell E.
APPLICANT: KLOETZER, William S.
APPLICANT: MAKAWIRA, Takehiko
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: Alexandria
STRTE: VIrginia
COUNTRY: United States
ZIP: Z2313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER IBM PC compatible
COMPUTER: IBM PC compatible
CONFUTENT SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
CLASSIFICATION: 424
ATTONNEY/ACENT INFORMATION:
NAME: Teskin L. Robin L.
REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REFERENCE/TOOKET NUMBER: 35,030
REFERENCE/TOOKET NUMBER: 35,030
TELECOMUNICATION INFORMATION:
TELECOMUNICATION SEG ID NO: 1:
SEQUENCE (FARACTERISTICS:
LENGTH: 390 base pairs
"VOR: MIGHEIC acid
                                                                                                                                                                                                                      US-08-264-093-5
US-10-039-785-56
US-09-273-839A-9
US-09-240-274-126
                                                                                                         US-09-240-274-133
US-09-240-274-132
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US-08-665-202-4
US-09-315-574-4
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LOCATION:
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172.8
172.8
169.2
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164.2
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December 29, 2003, 16:08:50 ; Search time 36.6551 Seconds (without alignments) 4009.823 Million cell updates/sec
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1 CAGTCTGCCCCGACTCAGCC......CCCGGTTGACCGTCCTAGGT 333
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.: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
.: /cgn2_6/ptodata/2/ina/pcTuS_COMB.seq:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-958-201-13
US-08-958-201-13
US-08-378-534
US-08-378-939-11
US-10-039-785-57
US-10-039-785-60
US-10-039-785-61
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US-09-702-702-970
US-09-702-702-970
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US-09-338-933-267
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                                                                                                                                                                                                                                                                                         569978 seqs, 220691566 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                              nucleic search, using sw model
                                                                                                                                                                          US-09-019-441-1_COPY_58_390
                                                                                                                                                                                                                                          IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                                                            Title:
Perfect score:
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2239.6
2225.8
2225.8
2225.8
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193.4
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                                                                                                                                                                                                             Sequence:
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Result No.

DB 3; Length 390;

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523
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Patent No. 6538938

GENERAL INFORMATION:

APPLICANT: Salcede et al.

APPLICANT: Salcede et al.

TITLE OF INVENTION: Receptors

FILE REFERENCE: PF550

CURRENT FILING DATE: 2002-04-05

PRIOR PILING DATE: 2002-04-06

PRIOR PILING DATE: 2001-12-20

PRIOR PILING DATE: 2001-11-14

PRIOR PILING DATE: 2001-11-14

PRIOR PILING DATE: 2001-11-14

PRIOR PILING DATE: 2001-11-09

PRIOR PILING DATE: 2001-11-09

PRIOR PILING DATE: 2001-11-09

PRIOR PILING DATE: 2001-10-09

PRIOR PILING DATE: 2001-09-21

PRIOR PILING DATE: 2001-09-22

PRIOR PILING DATE: 2001-06-04

PRIOR PILING DATE: 2001-06-05

PRIOR PILING DATE: 2001-06-05

PRIOR PILING DATE: 2001-06-06

PRIOR PILING DATE: 2001-06-07

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100.0%; Pred. No. 2.2e-95; ive 0; Mismatches 0;
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US-10-039-785-59
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333; Conservative
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Matches 33
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
CURRENT FILING DATE: 2002-05-07
PRIOR FILING DATE: 2002-04-05
PRIOR FILING DATE: 2001-11-2-20
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-0
PRIOR PLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-0
PRIOR PLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-10-0
PRIOR PLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-10-0
PRIOR PLICATION NUMBER: 60/329,473
PRIOR FILING DATE: 2001-08-02
PRIOR PLING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-05
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Best Local Similarity 90.7
Matches 302; Conservative
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                                                                                                                                                                CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTA 300
                                                                                                                                                                                                                        CAGGCTGAGGACGAGCTGATTATTACTGCAGCTCATATACAAGCAGCAGCAACACTTGGGTG 702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Specific binding members for estradiol, materials and methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
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Pred. No. 2.6e-77;
0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                    TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 333
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APPLICATION NUMBER: US 60/028,897
FILING DATE: 21-0CT-1996
INPORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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APPLICATION NUMBER: US/08/958,201
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/08958201; Patent No. 5977319; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Pope, Anthony R
APPLICANT: Pritchard, Kevin
APPLICANT: Williams, Andrew J
APPLICANT: Williams, Andrew J
APPLICANT: Johnson, Kevin S
TITLE OF INVENTION: Specific bir
TITLE OF INVENTION: materials an NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
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Best Local Similarity 89.2
Matches 297; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-958-201-13
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
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Pred. No. 1.1e-79;
0; Mismatches 31; Indels
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; OTHER INFORMATION: DNA encoding T1015E01 scFv
US-10-039-785-64
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CURRENT APPLICATION NUMBER: US/10/039,785

CURRENT PILING DATE: 2002-05-07

PRIOR APPLICATION NUMBER: 60/36,860

PRIOR APPLICATION NUMBER: 60/341,237

PRIOR FILING DATE: 2001-12-20

PRIOR APPLICATION NUMBER: 60/331,310

PRIOR FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-09

PRIOR FILING DATE: 2001-09

PRIOR FILING DATE: 2001-09

PRIOR FILING DATE: 2001-09

PRIOR FILING DATE: 2001-09-21

PRIOR PRIOR DATE: 2001-09-21

PRIOR PRIOR DATE: 2001-06-04

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 64, Application US/10039785 Patent No. 6538938
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ORGANISM: Artificial sequence
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Best Local Similarity 90.7
Matches 302; Conservative
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241 CAGGTTGAGGACGAGGCTGATTATTACTGAGCTCACTTACACGCAGAGTCAGTGATC 300
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APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Acceptors
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT APPLICATION NUMBER: 08/10/039,785
CURRENT APPLICATION NUMBER: 60/36,080
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR PRIOR APPLICATION NUMBER: 60/331,304
PRIOR FILING DATE: 2001-10-03
PRIOR PRIOR APPLICATION NUMBER: 60/327,364
PRIOR PRIOR APPLICATION NUMBER: 60/323,807
PRIOR PRIOR PLING DATE: 2001-00-01
PRIOR PILING DATE: 2001-00-03
PRIOR PILING DATE: 2001-00-03
PRIOR PILING DATE: 2001-00-04
PRIOR PILING DATE: 2001-06-04
PRIOR PILING DATE: 2001-06-05
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Pred. No. 1.1e-76;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                        TrcggaagagacccggTrgaccgTccTagGT 333
                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: DNA encoding T1014A04 scFv
US-10-039-785-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 54, Application US/10039785
Patent No. 6538938
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Best Local Similarity 88.99
Matches 296; Conservative
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181 CCTAATCGCTTCTCAGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 240
                                                                                                                                                                                                                                                         TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120
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                                                                                                                                                                                        CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTATACAACCAGTAGCACTTTGTTA 300
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Patent No. 5977319

GREERAL INFORMATION:
APPLICANT: Pritchard, Kevin
APPLICANT: Williams, Andrew J
APPLICANT: Williams, Andrew J
APPLICANT: Johnson, Kevin S
TITLE OF INVENTION: Specific binding members for estradiol;
TITLE OF INVENTION: materials and methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall_O'Toole Gerstein Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
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: 6300 Sears Tower, 233 South Wacker Drive
Chicago
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Pred. No. 8.4e-77;
0; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                                                               301 TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 Tregecegaegaecaagereacecerecrager 333
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLIANG DATE: 21-6CT-1996
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGENCE CHARACTERISTICS:
APPLICATION OF THE CHARACTERISTICS:
APPLICATION OF THE CHARACTERISTICS:
APPLICATION OF THE CHARACTERISTICS
APPLICATION OF 
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88.9%;
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CLONE: D12 (light chain)
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Best Local Similarity 88.9
Matches 296; Conservative
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CITY: Chicago
STATE: Illinois
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LOCATION:
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US-08-958-201-11
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241 CAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTA 300
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    TCCCCAGGCACGCCCCCCAAACTCATGATTTATGAGGTCAGTAATCGGCCCTCAGGGGTT 270

                                                                                                                   271 reraarcegricredecrecaagrerescaacacegecerecereacearcreseere 330
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                     301 TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 333
                                                                                                                                                                                                                                                                                                                                                             rrcegcegaeceaacercaecearceraeer 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .8e-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/08378939
Patent No. 5876961
GENERAL INPORMATION:
APPLICANT: LEWIS, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVARINO: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 272.2; Ded. No. 3.8e-0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D. C. STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFRENCE/DOCKET NUMBER: 1808-
TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 783-6040
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 902 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
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Best Local Similarity 88.6%;
Matches 295; Conservative
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TYPE: nucleic acid
STRANDEDNESS: both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
89.739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                              181 TCTGATCGCTTC
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LOCATION:
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LOCATION:
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; LOCATION:
US-08-378-939-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-08-378-939-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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88.9%; Pred. No. 1.2e-76;
                                     TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 333
                                                                                          703 Treececaceaceaceacercacercerectare 735
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OPERATING SYSTEM: DOS
CSTEMER: PSESSED for Windows Version 2.0
CSTERENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                       Sequence 23, Application US/09049672A
Patent No. 6155941
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY JAGET INFORMATION:
ATTORNEY JAGET INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/POCKET UNBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTR.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
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LENGTH: 891 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLLOGY: linear
IMMEDIATE SOURCE:
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Tang, Y. Tom
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                                                                                                                                                                                                                                                                                                                                                                                             Tang, Y. Tom
Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THYRNOT10
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Best Local Similarity
Matches 296; Conserv?
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; CLONE: 2872705
US-09-049-672A-23
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                                                                                                                                                                                                              US-09-049-672A-23
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APPLICANT:
APPLICANT:
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               CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC 180
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                                                                                    TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE NEFERENCE: PF550
CURRENT FILING DATE: 2002-05-07
PRIOR PAPLICATION NUMBER: 60/369,860
PRIOR PELING DATE: 2002-04-05
PRIOR PELICATION NUMBER: 60/313,31
PRIOR PELICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR PELICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-14
PRIOR PELICATION NUMBER: 60/331,044
PRIOR PELICATION NUMBER: 60/331,044
PRIOR PILING DATE: 2001-11-0-09
PRIOR FILING DATE: 2001-11-0-09
PRIOR FILING DATE: 2001-00-01
PRIOR PILING DATE: 2001-00-01
PRIOR PILING DATE: 2001-00-02
PRIOR PILING DATE: 2001-00-02
PRIOR PILING DATE: 2001-00-04
PRIOR PILING DATE: 2001-06-04
PRIOR PILING DATE: 2001-06-04
PRIOR PILING DATE: 2001-06-04
PRIOR PILING DATE: 2001-06-04
PRIOR PILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-06-07
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US-10-039-785-57
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Patent No. 6538938
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial sequence
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APPLICANT: Salcedo et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PFS50
CURRENT PAPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR APPLICATION NUMBER: 60/331,310
RRIOR FILING DATE: 2001-11-04
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-06-04
PRIOR SEQ ID NOS: 60
SOFTWARE: PALENTIN VET: 2.1
SEQ ID NOS: 60
SEQ ID NO 60
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                                                                                                              CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC
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US-10-039-785-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 60, Application US/10039785; Patent No. 6538938
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61 TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 120
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                                                                                               643 caggerigaggargaggergarrarracrecegercarargeaggaggaggararrreggre 702
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APPLICANT: Salcedo et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL

TITLE OF INVENTION: Receptors

FILE REFERENCE: PF550

CURRENT PILING DATE: 2002-05-07

CURRENT PILING DATE: 2002-06-05

PRIOR APPLICATION NUMBER: 60/341,237

PRIOR FILING DATE: 2001-12-20

PRIOR FILING DATE: 2001-12-20

PRIOR FILING DATE: 2001-11-04

PRIOR FILING DATE: 2001-11-04

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-10-09

PRIOR PILING DATE: 2001-10-09

PRIOR PILING DATE: 2001-10-09

PRIOR PILING DATE: 2001-00-09

PRIOR FILING DATE: 2001-00-09

PRIOR FILING DATE: 2001-00-09

PRIOR FILING DATE: 2001-00-09

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PRIOR PILING DATE: 2001-00-09
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                                                     241 CAGGCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTA
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77.9%; Score 259.4; DB 4
Best Local Similarity 86.2%; Pred. No. 3.7e-72;
Matches 287; Conservative 0; Mismatches 46
                                                                                                                                                                                                    703 rrcegeegagegaccaaegrcaccercerager 735
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US-10-039-785-61
                                                                                                                                                                                                                                                                                                                            Sequence 61, Application US/10039785 Patent No. 6538938 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                            -10-039-785-61
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                                                                                                                                                                               CAGGCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTA 300
                                                                                                                                                                                                                            CAGICITETEGRACIONAGECCOCCICAGITETETAGGICITECTAGACAGICAGITEACEAIC 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Salcade et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FITLE OF INVENTION: Receptors
FITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
PRIOR PELING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR PILING DATE: 2001-11-14
PRIOR PILING DATE: 2001-10-09
PRIOR PLING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR PILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR PILING DATE: 2001-06-04
PRIOR PILING DATE: 2001-06-04
PRIOR PILING DATE: 2001-06-05
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; OTHER INFORMATION: DNA encoding T1014B01 scFv
US-10-039-785-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 58, Application US/10039785
Patent No. 6538938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial sequence
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Best Local Similarity 86.2
Matches 287; Conservative
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US-10-039-785-58
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LENGTH: 735
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Wang, Tongtong
Bangur, Chaitanya
Lodes, Michael A.
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Vedvick, Tom
Carter, Darrick
Retter, Marc
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Best Local Similarity 92.03
Matches 266; Conservative
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US-09-702-705-970
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APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF550
CURRENT PILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2001-12-05
PRIOR FILING DATE: 2001-12-05
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-07
PRIOR PELING DATE: 2001-11-07
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-09-21
PRIOR PRILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR PRILING DATE: 2001-09-22
PRIOR PRILING DATE: 2001-09-24
PRIOR PRINCH PRILING DATE: 2001-09-24
PRIOR PRINCH                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACCCAGGCAAAGCCCCCCAAACTTGTGTTTATGAGGTCAGTAATCGGCCCTCAGGGGTT
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                                                   703 rrcegecegaegeaccaaegrcaccerceraegr 735
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US-10-039-785-55
                                                                                                                                                                                             Sequence 55, Application US/10039785 Patent No. 6538938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial sequence
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 55
LENGTH: 735
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APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Marc
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Ren, Liqun
TITLE OF INVENTION: DIAGNOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478614
CURRENT APPLICATION NUMBER: US/09/702, 705
CURRENT APPLICATION NUMBER: US/09/702, 705
CURRENT APPLICATION NUMBER: US/09/702, 705
SOFTWARE: FastSEQ for Windows Version 3.0
ILENGTH: 543
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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252.4 69.0 36.3 9 HSA528684 ADS86884 DONO 251.8 68.8 414 9 HST22X26 5 US7589 H.aapin 251.6 68.6 457 9 MMU57586 US7586 Macaca 250.6 68.3 354 9 HSA245015 AD5786 Macaca 249 68.0 486 9 AF417843 AF417843 HOMO 248.4 67.9 354 9 HSA45026 AD545026 HOMO 248.4 67.9 354 9 HSA45026 AD545026 HOMO 251.6 67.7 360 9 HUMICHVRN LISTORY HUMAN 252.6 67.7 375 9 HSA24502 AD54502 AD54502 HOMO 252.7 360 9 HUMICHVRN LISTORY HOMO 252.7 67.7 360 9 HUMICHVRN AD54502 AD54502 HOMO	32	. 23		412	17	AF452934	AF452934 Synthetic
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8 249.6 68.2 414 9 HSIGHXX23 X65905 H sapta 249 68.0 486 9 AF447843 AF477843 AF477843 HOMO 248.4 67.9 354 9 HSA245026 AJ245026 HOMO 248.6 67.8 423 9 HST14X12 Z75364 H sapta 248.6 67.7 360 9 HUMICHYRN LILIST LILIST HUMAN 247.6 67.7 350 9 HSMUSHYRN LILIST HUMAN AJ245023 HOMO 247.6 67.7 350 9 HSMA26203 AJ245023 HOMO 247.6 67.7 375 9 HSA245023	37	25		354	on I	HSA245015	15015 HOMO
9 249 68.0 486 9 AF417843 AF417843 AF417843 HOMO 248.4 67.9 354 9 HSA245026 AJ245026 HOMO 248.4 67.9 423 9 HST14X12 Z75364 H.sapi 248 67.8 435 9 MMUS7566 U57566 Macaca 3 247.6 67.7 360 9 HUMIGHVRN L12197 Human AJ245023 HOMO 247.6 67.7 375 9 HSA245023 AJ245023 HOMO 24765023 HOMO 247	38	49.		414	σ	HSIGHXX23	H.saple
0 248.4 67.9 354.9 HSAA45026 AJ245026 Homo 275364 H sapin 248 67.8 435.9 MMIGHVRN U57566 U57566 MGCaCa 247.6 67.7 360.9 HUMIGHVRN L 247.6 67.7 375.9 HSAA55023 AJ245023 HOMO 2 HO	39	24		486	σ	AF417843	343
1 248 67.8 423 9 HST14X12 Z75364 H.sapi 2 248 67.8 435 9 MMUSTPS6 US7566 MSG2Ca 3 247.6 67.7 360 9 HUMICHPRN L12197 HUMBAN 4 247.6 67.7 375 9 HSA245023 AJ245023 HOMO	40	48.		354	σ	HSA245026	126 Homo
2 248 67.8 435 9 MMU57566 U57566 Macaca 3 247.6 67.7 360 9 HUMIGHVRN L12197 Human 4 247.6 67.7 375 9 HSA245023 AJ245023 HOMO		4		423	σ	HST14X12	364 H.sapiens
3 247.6 67.7 360 9 HUMIGHVRN L12197 Human 4 247.6 67.7 375 9 HSA245023 A245023 A2245023 HOMO		4		435	σ	MMU57566	566 Macaca
4 247.6 67.7 375 9 HSA245023 AJZ45023 HOMO		7	٠.	360	σ	HUMIGHVRN	197
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AF416358 LOCUS LOCUS DEFINITION P ACCESSION A ACCESSION A KEYWORDS SOURCE ! : i p ORGANISM B M M M AUTHORS S		AF416358 435 bp mRNA linear PRI 27-MAR-2002	Papio cynocephalus anubis clone VH4-4 immunoglobulin heavy chain	variable region mRNA, partial cds.	AF416358	AF416358.1 GI:19744277	Papio anubis (olive baboon)	Papio anubis	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;	Cercopithecinae; Papio.	(bases 1 to 435)	Scinicariello, F., Jayashankar, L. and Attanasio, R.
	RESULT 1 AF416358			var					Buk	Marr	Cer	_	

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Papio cynocephalus anubis clone VH4-7 immunoglobulin heavy chain variable region mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trānslation="QVQLQESGPGLVKPSETLSLTCAVSGGSISGGFDWGWIRQPPGK
GLEWIGYIYGSSGSTNYNPSLKNRVTISKDTSKNQFSLKLSSVTAADTAVYYCARGSS
                                      Roubinet, F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGCCACCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 TCCCTGAAGCTGAGCTCTGTGACCGCCGCGCGCACACGGCCGTGTATTACTGTGCGAGAGGT
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                                                                    Variable region gene segment utilization in rhesus monkey hybridomas producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34) MO1. Immunol. 34 (3), 237-253 (1997)
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Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Ce.
University of Texas Southwestern Medical Center, 6000 Harry I
Blvd., Dallas, TY 75235-9140, USA
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                    1 (bases 1 to 363)
Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S.,
Blancher,A. and Capra,J.D.
                                                                                                                                                                                 2 (bases 1 to 363)
Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., and Capra,J.D.
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85.5%; Pred. No. 2.3e-67;
tive 0; Mismatches 50; Indels
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/organism="Macaca mulatta"
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    Cercopithecinae; Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="MKHLWFPLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVS
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SSVTAADTAVYYCARDLGAYNWGPQHYWGQGVLVTVSSASASA"
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Baboon immunoglobulin variable region heavy chains: identification of genes homologous to members of the human IGHV1-IGHV7 subgroups Immunogenetics 53 (10-11), 815-820 (2002)
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Macaca mulatta
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                                                                                                                                                                                                                                                     /product="immunoglobulin heavy chain variable region"
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                                                                                                 2 (bases 1 to 435)
Scinicariello,F., Jayashankar,L. and Attanasio,R.
Direct Submission
Submitted (04-SEP-2001) Department of Biology, Ge
University, PO BOX 4010, Atlanta, GA 30302, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.2%; Score 271.6; DB 9
85.8%; Pred. No. 7.8e-68;
iive 0; Mismatches 49
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U57559.1 GI:1575065
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GGSISSGYYWGWIRQPPGKGLEWIGNIDGNSASTNYNPSLKORYTISKDTSKNQFSLK
GSSTSAGYYWGARDWTYSGNYKYGLDAWGQGVVVTVSSASAS"
125 c 127 g 95 t
                                                                                                                                                                                                                            Scinicariello, F., Jayashankar, L. and Attanasio, R.
Baboon immunoglobulin variable region heavy chains: identification
of genes homologous to members of the human IGHV1-IGHV7 subgroups
Immunogenetics 53 (10-11), 815-820 (2002)
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                                                                                    Papio anubis
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Papio.
1 (bases 1 to 441)
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protein id="AAL96425.1"
db_xref="GI:19744280"
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                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 441)
Scinicariello,F., Jayashankar,L. and Attanasio,R.
Direct Submission
Submitted (14-SEP-201) Department of Biology, Ge
University, PO BOX 4010, Atlanta, GA 30302, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .441
/organism="Papio anubis"
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/sub_species="anubis"
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/clone="VH4-7"
                                                            anubis (olive baboon)
   AF416359.1 GI:19744279
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/gene="IGHV4-4"
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GLEMIGEIXHSGSTRYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCASDSYY
BFWSGKGVWGQGTLVTVSS"
                                                                                                                                                                                                                                                                                                                    B lymphocytes, the splenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (11-JAN-2000) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna benzi 10- Genova,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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J. Immunol. 164 (11), 5596-5604 (2000)
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85.2%; Pred. No. 6.6e-67;
iive 0; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                         egion, partial, clone CD27low-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="IgD-low SE
/tissue_type="tonsil"
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/clone="CD27low-2"
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                                                                                                  IgM; IgM heavy chain;
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                                                                                                                                             Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 363)
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1. ..420

/codon start=1

/poduct=immunoglobulin heavy chain"

/protein id="AACO2637.1"

/db_xref="G1:1575068"

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GYSISSGQYGNWIRQPPGKGLEWIGSIGGSRGNTNHNPSLKSRVTISIDTSKNQFSLK

GRISLTAADTAUFYRADGGYSSRFPDYWGQGVLVTVSS"

128 c 121 g 95 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA linear PRI 11-FEB-1998
chain variable region, anti-RBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cercopithecinae; Macaca.

1 (Dases 1 to 420)
Andris,J.S., Miller,B., Abraham,S.R., Cunningham,S., Roubinet,F.,
Blancher,A. and Capra,J.D.
Variable region gene segment utilization in rhesus monkey
hybridomas producing human red blood cell-specific antibodies:
predominance of the VH4 family but not VH4-21 (V4-34)
MOL Immunol. 34 (3), 237-253 (1997)
                                                                                                                                                               241 TCCCTGAACCTGAACTCTGTGACCGCGGGGACACGGCCGTGTATTACTGTGCCAGAGAT 300
                                                                                                                                                                                                238 rcccrdaagcrdagcrcrdrdacgccccccccccccccrcrarracrcrcrcaagaga 297
                                                                                                                                                                                                                                                       298 ATCCGGATGACTACGGCACCTCTTGACTACGGGGCCAGGGAACCCTGGTCACGTC 357
                                                121 cccccadedaaddacricaagredarredagaaarcrarcara---Gregaagcaccaac 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 420)
Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
and Capra, J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission Submission Submitted (06-NAY-1996) J.S. Andris, Molecular Immunology Center, Submitted (06-NAY-1996) J.S. Andris, Molecular Immunology Center, University of TX53SS-1940, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CAGCTGCAGCTGCAGGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC 60
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                               CCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGGCCCACCAAC
                                                                                                                                                                                                                                           301 TGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACGTC
                                                                                       TACAACCCGTCCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 420;
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Pred. No. 1.9e-66;
0; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca mulatta Ig rearranged heavy and property macaca mulatta partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Macaca mulatta"
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/db_xref="taxon:9544"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macaca mulatta (rhesus monkey)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="hybridoma 108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:1575067
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Best Local
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AUTHORS
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AUTHORS
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MMU57560
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                                                                                                                                                                                                                                   363 bp DNA linear PRI 19-FEB-1997
Human immunoglobulin heavy chain variable region (V4-4b) gene,
partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /trānslation="QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSNWMSWVRQPPGK
GLEWIGEIYHSGSTNYNPSLKSRVTISVDKSKNQFSLKLSSVTAADTAVYYCARGIPH
DYGTLFDYWGQGTLVTVSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glas, A.M., Nottenburg, C. and Milner, E.C.B.
Direct Submission
Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
1000 Seneca Street, Seattle, WA 98101, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Η;
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                                      TGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTC 360
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 363)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glas, A.M., Nottenburg, C. and Milner, E.C. Analysis of rearranged immunoglobulin heavy chain variable region genes obtained from a bone marrow transplant (BMT) recipient Clin. Exp. Immunol. 107 (2), 372-380 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCCTGAAGCTGAGCTCTGTGACTGCCGCAGACACGGCCGTGTATTACTGTGCCAGCGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="immunoglobulin heavy chain variable region"
/protein_id="AAC51094.1"
/db_xref="G1:1791201"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <1. >363
/gene="V4-4b"
/note="Ig VH4 heavy chain"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="14"
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Best Local Similarity
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Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC
אורקיבים mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | TCCCTGAACCTGAACCCCTGGACCGCGCGCGCACACGCCGTGTATACTGTGCCAGAG-- 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ACCTGCGCTGTCTCTGCTGCTCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACAACCCGTCCATCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 GATAGTGGTAGTTATCCGTGATAATTCATTGGATGTCTGGGGCCGGGGAGTTCTGGTC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
2 (bases 1 to 373)
Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A. and Capra, J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata, Vertebrata, Euteleostomi,
Catarrhini, Cercopithecidae,
                                                             /gene="CDR1"
/note="complementarity-determining region 1; putative"
                                                                                                                                                                                      putative"
                                                                                                                                                                                                                                                                                        region 3; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGGTACAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAAGCCCTCGGAGACCCTGTCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTATGGTAGTGGTGGGGGGCACCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Variable Region Gene Segment Utilization in Rhesus Monkey
Hybridomas Producing Human Red Blood Cell-Specific Antibodies:
Predominance of the VH4 Family but not VH4-21 (V4-34)
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9
                                                                                                                                                                                                                                                                                                                                                                        Length 1359;
                                                                                                                                                                   /note="complementarity-determining region 2;
298. .339
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                        /gene="CORR3"
/note="complementarity-determining
/note="complementarity-determining
                                                                                                                                                                                                                                                                                                                                                                  Query Match 72.9%; Score 266.8; DB 9; Best Local Similarity 84.4%; Pred. No. 2e-66; Matches 314; Conservative 0; Mismatches 52;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
Cercopithecinae; Macaca.
1 (bases 1 to 373)
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                                                                                                                                                                                                     298. .339
/gene="CDR3"
298. .339
  91. .108
/gene="CDR1"
91. .108
                                                                                                                                       151. .201
/gene="CDR2"
                                                                                                                      /gene="CDR2"
151. .201
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                                                                                                       151. .201
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Best Local Similarity
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DKRVEIKTGCGSKPPRCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
SQEDPDVKFNWYNGAEVHHARETQYNSTYRVVSLTVTHQDMLNGKEYTCKVSNKAL
PAPLQKTISKDKGQPREPQVYTLPPSSEELFKNQSLTCLKKGFYPSDIVVEMESSGG
PENTYKTTPPVLDSDGSYFLYSKLTVDKSRNQQGNVFSCSVMHBALHNHYTQKSLSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/product="immunoglobulin_gamma"
/protein_id="AAA18103.1"
/db_xref="G1:29119"
/tb_xref="G1:29119"
/translation="QVQLQESGPGLVKPSETLSLTCAVSGGSISSAYDWSWIRQPPGKGLWRINGERINGSTSYNPALTSTREAMGUSEKLSSYTAADTAVYCARGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear PRI 13-MAY-1994
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                                                                                                                                                                     CCCCCAGGAAGGGGCTGGATTGGGTCTATCGGTGGTAGTCGTGGTAACACCAAC 237
                                                                                                                                                                                                                                                    CACAACCCCTCCTCAAGAGTCGAGTCACCATTTCAATAGACACGTCCAAGAACCAGTTC 297
                                                                                                                                                                                                                                                                                                             TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGAT 300
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                                                                                                     ACCTGCGCTGTCTCTGGTTACTCCATCAGCAGTGGTTATGGCTGGAACTGGATCCGCCAG 177
                                                                                                                                                                                                                                                                                                                                                                                                                     358 GGGGGTACAGTTCCCG---GTTCTTTGACTACTGGGGCCAGGGAGTCCTGGTCACGGTC 414
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Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.

1 (bases 1 to 1359)
Lewis, A.P., Barber, K.A., Cooper, H.J., Sims, M.J., Worden, J. and
CCCCCAGGGAAGGGACTGGATTGGACGTATCTCTCTGGTAGTGGTGGGCCACCAAC
                                                                                                                                                                                                                            TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source text: Macaca fascicularis cDNA to mRNA.
Location/Qualifiers
1. .1359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macaca fascicularis imunnoglobulin gamma variable regregion, complementarity-determining region 1 (CDR1), complementarity-determining region 2 (CDR2), complementarity-determining region (CDR2) mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cloning and sequence analysis of kappa and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dev. Comp. Immunol. 17 (6), 549-560 (1993) 94131152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Macaca fascicularis"
/mol_type="mRNA"
/db_xref="taxon:9541"
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L13307.1 GI:293118
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SOURCE

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HSUB0180 368 bp DNA linear PRI 19-FEB-1997 Human immunoglobulin heavy chain variable region (V4-4b) gene,
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GLEWIGEIYHSGSTNYNPSLKSRVTISVDKSKNQFSLKLSSVTAADTAVYYCARDWAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accrececrerereregrescreearcacaearacaeracresresasarreserececeas 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 TACAACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACAAGTCCAAGAACCAGTTC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 ATGGCGATTTTTGGAGTGGTTATTATGTTCGGGTACTGGGGCCCAGGAACCCTGGTCACC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 TGGGCCCAAAT---AGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACC 357
                                                                                                                                                                                Istituto Nazionale per la Ricerca
L.go Rosanna benzi 10- Genova,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="immunoglobulin mu heavy chain variable region"
/protein_id="CAB66350.1"
/db_xref="G1:6723538"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="immunoglobulin mu heavy chain variable region" 98 c 114 g 79 t
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                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/chzomosome="14"
/clone="CD27low-8"
/call_type="Ig0-low SE B-lymphocyte"
/rearranged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.0%; Score 263.4; DB 9;
85.9%; Pred. No. 1.9e-65;
J. Immunol. 164 (11), 5596-5604 (2000)
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                                                                                                                                                                                                                                                                                                                            1. ...organism="Homo sapiens"
/organism="Homo sapiens"
                                                                                                                                                      Direct Submission
Submitted (11-JAN-2000) Dono M.,
sul Cancro, Immunologia Clinica,
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/gene="IGHV4-4"
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/gene="IGHV4-4"
                                                                                            (bases 1 to 366)
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                                                                                                                                Dono, M.
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AJ279520 AJ279520 GI:6723537 IGM; igM heavy chain; immunoglobulin mu heavy chain; variable region.
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Chiorazzi,N. and Ferrarini,M.
Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
marginal zone equivalents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /trānslation="WVLSQVQLQESGPGLVKPSETLSLTCAVSGYSISSGYGWSWIRQ
PPGKGLEWIGYIVVNSGSTDYNPSLKSRVTISKDTSKNQFSLKLSSVTAADTAVYYCA
RARRGSSYVDYWGQGYLVTVSS"
109 c 114 g 78 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCCTGAACCCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGAT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 Accrecerererereracrecareacadagerarageragacrecaeracarecede 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
         and Capra, J.D.

Bloed: Submission
Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
University of Texas Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 75225-9140, USA
Location/Qualifiers
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred..No. 4.3e-66;
0; Mismatches 49; Indels
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/db_xref="G1:1575064"</pre>
                                                                                                                                                                                                                         /organism="Macaca mulatta"
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/db_xref="taxon:9544"
/note="hybridoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 72.6%;
Best Local Similarity 85.0%;
Matches 311; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
Homo sapiens
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1. .420
/codon start=1
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/producf="immunoglobulin heavy chain"
/protein_id="AAC02642.1"
/db_xref="G1:1575078"
/dc_xref="G1:1575078"
/dc_xref
                                                                                                                                                                                                                      ימיוט / המל 1 mRNA linear PRI 11-FEB-1998
Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC
antibody, mRNA, partial cds.
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298 AGGGTATTGTAGTAGTACCAGCTGCAAAATTTGACTACTGGGGCCAGGGAACCCTGGTCA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 420)
Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
and Capra, J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Abraham, S.R., Cunningham, S., Roubinet, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
University of Texas Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 75255-9140, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cercopithedinae; Macaca.

1 (bases 1 to 420)
Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Roubinet Blancher, A. and Capra, J.D.
Variable region gene segment utilization in rhesus monkey hybridomas producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34)
Mol. Immunol. 34 (3), 237-253 (1997)
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Catarrhini; Cercopithecidae;
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84.2%; Pred. No. 4.7e-65;
ive 0; Mismatches 55; Indels
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/organism="Macaca mulatta"
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/db_xref="taxon:9544"
                                                                                                                                                                                                                                                                                                                                                                                                                               Macaca mulatta (rhesus monkey)
Macaca mulatta
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Mammalia; Eutheria; Primates;
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                                                       CCGTCTCCTCA 366
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Best Local Simi
Matches 308;
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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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PUBMED
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MMUS7565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glas, A.M., Nottenburg, C. and Milner, E.C.B.
Direct Submission
Submitted (29-NOV-1996) Immunology; Virginia Mason Research Center, 1000 Seneca Street, Seattle, WA 98101, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="QVQLQESGPGLVKPSGTLSLTCAVSGGSISSSNWWSWVRQPPGK
GLEWIGEIYHSGSTNYNPSLKSRVTISVDKSKNQFSLKLSSVTAADTAVYYCARDRVL
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[ bases 1 to 368)
Glas, A.M., Nottenburg, C. and Milner, B.C.
Analysis of rearranged immunoglobulin heavy chain variable region genes obtained from a bone marrow transplant (BMT) recipient Clin. Exp. Immunol. 107 (2), 372-380 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="CD19+ B cells"
/tissue_type="peripheral blood"
/note="CD19+ peripheral blood B cells obtained from a
healthy subject; clone 105 in reference 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="immunoglobulin heavy chain variable region"
protein_id="AAC51095.1"
db_xref="GI:1791203"
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Pred. No. 2.4e-65;
0; Mismatches 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="V4-4b"
/note="Ig VH4 heavy chain"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'mol_type="genomic DNA"
'db_xref="taxon:9606"
'chromosome="14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 map="14q32-q33"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="tt3a6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .309
/gene="V4-4b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.9%;
85.7%;
partial cds.
U80180
U80180.1 GI:1791202
                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 368)
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Dono,M., Zupo,S., Leanza,N., Melioli,G., Fogli,M., Melagrana,A., Chiorazzi,N. and Ferrarini,M. Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic marginal zone equivalents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon start=1
/product="immunoglobulin mu heavy chain variable region"
/product="immunoglobulin mu heavy chain variable region"
/protein_id="CAB44166.1"
/db xref="G1:495523"
/translation="QVQLQBSGPGLVKPSGTLSLTCAVSGGSISSSNWWSWVRQPPGK
/translation="QVQLQBSGPGLVKPSGTLSLTCAVSGGSISSSNWWSWVRQPPGK
GLEWIGSIYYSGSTYYNPSSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARHEYS
                                                                                                                                                                                                                                                                                                                                                                                                          PRI 01-JUN-2000
variable
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Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna benzi 10- Genova,
                                                                                                                                    295 TCCCTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCGGAGGTAT 354
                                                                                                                                                                                                                175 CCCCCAGGGAAGGGACTGGAGTGGATTGGACGTTTCTATGGTACTAGTGGGAGCACCTAC 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                          241 TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGAT
                                                                                                                                                                                              301 TGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCCAGGGAGTCCTGGTCACCGTC
                                        181 TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AJ245032.1 GI:4995522
IgM; IgM heavy chain; immunoglobulin mu heavy chain; variable
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens mRNA for immunoglobulin mu heavy chain region, partial, clone 1-F24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="B-lymphocyte"
/tissue_type="tonsil"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .363
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <1. .>363
/gene="IGHV4-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l. .363
/gene="IGHV4-4"
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 c
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Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecidae; Macaca.

1 (bases 1 to 411)
Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Roubinet,F.,
Blancher,A. and Capra,J.D.
Blancher,A. and Capra,J.D.
Variable region gene segment utilization in rhesus monkey
hybridomas producing human red blood cell-specific antibodies:
predominance of the VH4 family but not VH4-21 (V4-34)
MO1. Immunol. 34 (3), 237-253 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /trānslation="WKHLWFPLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVS
GGSISSNYWSWIRQPPCKGLEWIGRFYGTSGSTYYNPSLTSRVTISTDTSKNQFSLKL
SSYTAADTAVYZCARYTVSKAFDYWGGGVLVTVSS"
124 C 115 g 91 t
                                                                                                                                                                                                                                                                                                PRI 11-FEB-1998
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                                                                                                                                                                                                                                                                                  wMU57563 411 bp mRNA linear PRI 11-FEB-1996
Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC
antibody, mRNA, partial cds.
                                                                              58 CAGGTGCAGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
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      TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGAT 300
                          295 TCCCTGAAGGTGAGCTCTGTGACGCCCCGGGACACGGCCGTGTATTACTGTGCGAGAGAGG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 411)
Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
and Capra, J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 Accrececrereregreere---carcacagraacracresacresarresecre 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
University of Texas Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 75235-9140, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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/prodoct="immunoglobulin heavy chain"
/protein_id="AAC05490.1"
/db_xref="GI:1575074"
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86.3%; Pred. No. 8.1e-65;
ive 0; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. 411
/organism="Macaca mulatta"
/mol_type="mRNA"
/db_xref="taxon:9544"
/note="hybridoma 1B4"
                                                                                                                                                                                                                                                                                                                                                                                                            Macaca mulatta (rhesus monkey)
Macaca mulatta
                                                                                                                                                                                                                                                                                                                                                                          U57563.1 GI:1575073
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Matches 316; Conserv
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GTCTCCTCA 423
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H.Sapiens mRNA for XLA IG heavy chain VDJ region (LE 4-8).
K565910 S58679
K65910.1 G1:395108
diversity region; Ig heavy chain; immunoglobulin; joining region; variable region.
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Homo sapiens
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 423)
Schiff, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bone marrow cells in X-linked agammaglobulinemia express pre-B-specific genes (lambda-like and V pre-B) and present immunoglobulin V-D-J gene usage strongly biased to a fetal-like
                                                                               1 CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGGGACCCTGTC
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                                Gaps
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Submitted (08-APR-1992) C. Schiff, Centre D'Immunologie de Marseille, Case 906, 13288 Marseille, Cedes 9, FRANCE (bases I to 423)
Millil, M., Le Doist, F., de Saint-Basile, G., Fischer, A., Fougereau, M. and Schiff, C.
                                3;
   Length 363;
                                Indels
 Score 260.4; DB 9;
Pred. No. 1.4e-64;
0; Mismatches 56;
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Query Match
Best Local Similarity 83.9%;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecidae;
Losaes i to 41 Macaca.

Losaes i to 41 Macaca.

Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Roubinet,F., Bancher,A. and Capra,J.D.

Bancher,A. and Capra,J.D.
Variable region gene segment utilization in rhesus monkey hybridomas producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34)

MOL. Immunol. 34 (3), 237-253 (1997)
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Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC
antibody, mRNA, partial cds.
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Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
and Capra, J.D.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                      181 TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC
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                            378. .423
/note="joining region"
120 c 123 g
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Search completed: December 29, 2003, 19:01:25 Job time : 1517.15 secs

Title: Perfect score:

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Sequence:

Scoring table:

Searched:

Database

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CE 1 (bases 1 to 453)
SIN H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
AL Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: M.G. Clone distribution information can be found through the I.M.A.G. E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
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UI-HF-BKO-aal-c-02-0-UI.rl NIH MGC_36 Homo sapiens cDNA clone
IMAGE:3053955 5', mRNA sequence.
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LOCUS
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     BQ072430 AGENCOURT
BU429270 UI-HF-BN0
CB551642 MMSP0006
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5616.780 Million cell updates/sec
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                                                                                                                                                                                                     December 29, 2003, 16:08:50 ; Search time 1583.73 Seconds
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1 CAGCTGCAGCTGCAGGAGTC.....TCCTGGTCACCGTCTCCTCA 366
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                                GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 1.0
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 524)

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UI-HF-BN0-aeq-c-02-0-UI.rl NIH_MGC_50 Homo Bapiens CDNA clone
IMAGE:3065067 5', mRNA sequence.
68.1%; Score 249.2; DB 13; Length 1036; 83.9%; Pred. No. 4.4e-55; tive 0; Mismatches 53; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BU429270.1 GI:22767757
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Homo sapiens
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_6839001 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5761604
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        301
        TGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACGTC.
        360

        335
        ACGGGCTATATAGTGGGTACCCCCTTTGACTAGGGGCCAGGGAACCCTGGTCACCGTC
        394

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1036)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   э;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 453;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.2%; Score 271.6; DB ilarity 85.8%; Pred. No. 4e-61; Conservative 0; Mismatches 4
                                                                                        organism="Homo sapiens"
              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BQ072430.1 GI:19901476
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BQ072430
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Matches 314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTA---ACTGGTGGACCTGGATCCGC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 ACCTGCACTGTCTCTGGTGGCTCCATCAGCAGTAGTTACTTCTGGGGCTGGATCCGC 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCTCCCTGAACCTGAACTCTGTGACCGCGGGGACACGGCCGTGTATTACTGTGCCAGA 297
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//olde="Vectors: pTy73-pec; Site 1: Not1; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(3.5-4.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "
                                                         Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Ecol RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbry/image/image.html
Seq primer: M13 Forward.
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   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol type="mtNA"
/mol type="mtNA"
/db_xref="taxon:9606"
/clone="IMAGB:3065067"
/tissue_type="lymph"
/cell_type="graminal center B cells"
/cell_line="WGC85"
/lab_host="DH10B (LTI)"
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Pred. No. 9.9e-55;
0; Mismatches 46
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Best Local Similarity 84.5%;
Matches 317; Conservative
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VERSION
KEYWORDS
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EST 01-JUN-2003

CB551642 680 bp mRNA linear E:
MMSP0006\_D02 MMSP Macaca mulatta cDNA, mRNA sequence.
CB551642\_
ES51642.1 GI:31300837
EST.

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BX283435
BX283435 NIH MGC 48 Homo sapiens cDNA clone IMAGp958G051281 ;
IMAGE:4565020, mWA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 502)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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Katze,M.G., Bumgarner,R., Korth,M., Feldman,R., Amjadi,M.
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                                                                                                                                                                                                                                                                            University of Washington
Box 158070, Seattle, WA 98195-8070, USA
Tel: 206 712 6156
Fax: 206 712 6055
Email: ted@locke.hs.washington.edu
Similar to GenBank entry AF062240 AF662240 Homo sapiens
23u-44 immunoglobulin heavy chain variable region (IGH)
partial cde. 5/2001
Plate: MMSP006 row: D column: 02.
Location/Qualifiers
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                                                                                                                                                                      Expressed sequence tags from Rhesus macaque spleen
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/dev_stage="adult"
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187 c 177 g
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/db_xref="taxon:9544"
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BX283435.1 GI:28847889
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                                                                                                                                                                                                                                  Contact: Holzman T
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mRNA sequence.
BG397580
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Best Local 9
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ORIGIN
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AUTHORS
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BG397580
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                                                                                                                                                                                                                                                                                                                                                                                                            /tissue type="primarry B-cells from tonsils (cell line)"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GCACGAGG(6). Size-selected >SObbp for average insert size 1 8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                               RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/ehowLib.pl.cgi/response?libNo-972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 111
Fax: +49 30 32639 111
                                                                  GmbH
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                                                Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung
IN Rowenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGD958G051281.
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                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp958G051281 ; IMAGE:4565020"
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 Radelof, U., Schneider, D. and Korn, B.
                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
             Human UnigeneSet - RZPD3
Unpublished
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BG397580 862 bp mRNA linear EST 12-MAR-2001
602438620F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565020 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 862)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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                                                                                                                                                                                                                                                                                                                                          Email: cgapbe-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lclound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
g column: 05
High quality sequence stop: 827.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                         BG397580.1 GI:13291028
                                                                                                                                    Homo sapiens (human)
Homo sapiens
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AGENCOURT 8495271 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6302029
5', mRNA Sequence.
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   35 TICTCCCTGAGGCTGAGCTCTGTGACCGCCGCGACACGCCCGTGTATTACTGTGCGAGT 414
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Sass 1 to 921)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                       415 GGTTGTAGTGGTGATAGCTGCTTGCCTTTGACTACTGGGGGCCAGGGAACCCTGGTC
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http://image.llnl.gov
Plate: LLCMX518 row: n column: 14
High quality sequence start: 10
High quality sequence stop: 604.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.

    .921
    /organism="Homo sapiens"

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/clone_lib="Homo sapiens PLACENTA_COT_5-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA_COT_5-NORMALIZED"
/note="Ist actand cDNA was primed with a NoLI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
231 c 231 g 177 t
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374 CTGGGAGACATCTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTC 433
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
eggl-bin/cluster.cg1?seq-CS0A1086CE07QPl&cluster=7198.r. Contact:
Forg Liang Email: fliangelifetech.com URL:
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOA1086CE07QPl.
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Li.W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                 BX324929 mRNA
BX324929 Homo sapiens PLACENTA COT 25-NORM
clone CSODI086YJI3 5-PRIME, mRNA sequence.
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Genoscope - Centre National de Sequencage
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/db_xref="taxon:9606"
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BX324929.1 GI:30338413
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ACCTGCCCTGTCTCTCTCTCTCTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG
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/tissue_type="primary B-cells from tonsils (cell line)"
/issue_type="primary B-cells from tonsils (cell line)"
/issue_type="Drimary B-cells from tonsils (cell line)"
/clone line="NHH MGG 48"
/clone line="NHH MGG 48"
/note="Organ: B-cells, Vector: pOTB7; Site_1: XhoI;
Site_2: EccRI; cDNA made by Oilgo-dT priming.
Directionally cloned into EccRI/XhoI sites using the following 5' adaptor: GGGAGAGG(6). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: Libis is a NIH MGC Library."
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602637281F NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4764956 5',
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                         TICTCCCTGAACCTGAACTCTGTGACCGCGGGGACACGGCCGTGTATTACTGTGCCAGA 297
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 867)
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov a column: 21
High quality sequence stop: 637.
Location/Qualifiers
 AACTACAACCCGTCCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAG
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Best Local Similarity 82.8%; Pred. No. 1.2e-53;
Matches 303; Conservative 0; Mismatches 59;
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/db_xref="taxon:9606"
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BG685428
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AGENCOURT_8485057 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301263 5', mRNA sequence.
BQ710876.1 GI:21849775
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                                                                        TCCCTGAACCTGAACTCTGTGACCGCCGCGCGCCGTGTGTTTACTGTGCCAGAGAT 300
                                                                                                                                                                        318 TCCCTGAAGCTGAGGTCTGTGACCGCGGGGACACGGCCGTGTATTACTGTGCAGAGTCT 377
                                                                                                                                                                                                                                                                                   cccccaggaaagggcrrgagrrggarrgggaaarcrarcaragrg--ggagcacacaac 257
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM216 row: n column: 16
High quality sequence stop: 560.
                                                TACAACCCGTCACAGAGTCGAGTCATTTCACAAGACACGTCCAAGAACCAGTTC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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09

Gaps

9

297

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/orgānism="Homo sapiens"
/clone="DKFZp666M10119"
/clone=lib="686 (synonym: hlcc1). Vector pSportl_Sfi; host
DH108; sites Sfils + Sfils"
/dev_stage="adult"
/tissue_type="cDNA-collection"
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939 bp mRNA linear EST 16-JUL-2002
AGENCOURT 8495323 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301745
5', mRNA sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2518 row: b column: 18
High quality sequence start: 12
High quality sequence stop: 587.
Location/Qualifiers
1. 939
                                                                                                                                                                                                                                                                                                                                                                                          61 ACCTGCGCTGTCTCTGTGGCTCTGTCAGCAGT - - AGTAACTGGTGGACCTGGATCCGC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                     Length 532;
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                                                                                                                                                                                                  Sequence 532 BP; 108 A; 163 C; 142 G; 114 T; 5 other;
                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                       903
                                                                                                                                                                                                                                                     Score 241.6; DB 2
Pred. No. 3.4e-53;
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
/mol type="mRNA"
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82.1%;
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33; Conservative
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Matches 303;
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Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                       258 TACTACAACCCGTCCCTCAAGAGTCGAGTCACCATATCCGTAGACACGTCCAAGAACCAG 317
                                                                                                                                                                             ACCTGCGCTGTCTCTGTGGCTCTGTCAGCAGTAGTA---ACTGGTGGACCTGGATCCGC 117
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Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
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81 sequence also available.
This clone (DKFZp686M10219) is available at the RZPD in Berlin.
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                       59; Indels
82.4%; Pred. No. 2.3e-53;
ive 0; Mismatches 59
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UI-HF-BLO-aco-h-03-0-UI.r1 NIH MGC_37 Homo sapiens cDNA clone
IMAGE:3059933 5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seg primer: M13 Forward.
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llarity 90.2%; Pred. No. 1.3e-52;
Conservative 0; Mismatches 26
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                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                               Location/Qualifiers
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                                                                                                                               /clone="INAGE: 331745"
/lab_host="INAGE: 331745"
/lab_host="DH10B (phage-resistant)"
/clone=lib="NHH MGC_l13"
/clone=lib="NHH MGC_l13"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
inco EcoRI/AhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superseript II RT (Life Technologies). Note: this is a
NIH MGC Library."
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NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Parayed by: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
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Pred. No. 6e-53;
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                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                 /mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:3059931"
/tissue type="taxon:9606"
/clone="IMAGE:3059931"
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/cell_tine="MGG55"
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/note="Vector: pT713-Pac; Site_1: NotI; Site_2: Eco RI;
/note: pT713-Pac; Site_1: No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGCCCCCAAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGCCACC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 AACTACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAG 237
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BX337642 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI044YB21 5-PRIME, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1058)
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84.0%; Pred. No. 2e-52;
ive 0; Mismatches 44; Indels 15
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                             organism="Homo_sapiens"
                                                            Location/Qualifiers
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                              Seg primer: M13 Forward
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BX337642 Homo
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/close lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMYSPORT 6 vector. Library was normalized.
327 c 283 g 216 t 18 others
                                                                                                                     http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODIO44CAllQPl&cluster=7198.r. Contact
gri-bin/cluster.cgi?seq=CSODIO44CAllQPl&cluster=7198.r. Contact
Feng Liang Email : fliangelifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIO44CAllQPl.
Location/Qualifiers
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
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                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
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/clone="CS0DI044YB21"
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ilarity 81.1%;
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Best Local Similarity
Matches 309; Conserv
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Anti-CD4 antibody Monkey anti-CD4 he DNA encoding cynom Human diagnostic a

Heavy chain DNA fr

Human lung cancer

ebvHigM MSI19D10 h

Human monoclonal

Nuclectide sequenc Anti-CD40 monoclon EST clone 099. Ho Germline anti-IGF-Monkey anti-human Monkey anti-human

Scoring table:

Searched:

Database

Perfect score:

Run on:

Sequence:

Anti-CD4 antibody
Multiple sclerosis
Human bladder tumo
Human immunoglobul
Human LH11238 mono
PAMZ single chain

Human immune syste Anti-IGF-IR antibo

Primatised anti-hu Macaque primatized DNA sequence of a MAb 1-3-1 variable Human antibody clo DNA-1 related to h Human immune syste DNA encoding anti-DNA encoding human DNA encoding human

Human PTHrP monoc

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Anti-human CD23 6G5 moclonal antibody heavy chain variable region DNA.
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/product= "anti-human CD23 6G5 heavy chain variable
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note= "CDS does not contain a stop codon"
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ABT31871
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Primatised anti-hu
Macaque primatized
DNA sequence of a
Nucleotide sequenc
Human gamma-4 heav
Human gamma-4 beav
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                                                                                                          December 29, 2003, 16:08:50 ; Search time 159.688 Seconds (without alignments) 6187.013 Million cell updates/sec
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:
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                GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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AAT62513 standard; DNA; 1431

AAT62513

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/*tag= e
/note= "encodes CDR 2 region"
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                                                                                                                                                                                                                                                   Reff ME;
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 misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 DNA sequences (AAT62512 and AAT62513) respectively code for primatised forms (AAW01821 and AAW01822) of the light and heavy of cynomolgus monkey anti-human B7.1 antigen moncolonal antibody of cynomolgus monkey anti-human B7.1 antigen moncolonal antibody 16C10. Cloned 16C10 light and heavy variable genes are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constant region genes to allow prodn. of primatised antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1 antibodies have also been produced (see also AAW01817-20). The primatised antibodies inhibit the B7:CD28 pathway, making them unseful immunosuppressants for the treatment of autoimmune disorders and graft-versus-host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -useful for treating autoimmune disease or graft-versus-host disease
                                                                                     Primatised anti-human B7.1 antigen antibody 16C10 heavy chain DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.0%; Score 256.2; DB 18; Length 1431; 82.2%; Pred. No. 6.1e-61; ative 0; Mismatches 53; Indels 15;
                                                                                                                    Monoclonal antibody; cynomolgus monkey; macaque; 16C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic luque erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shestowsky WS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanna N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Fig 10B; 81pp; English.
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                                                                                                                                                                                                                                                                          Chimeric Homo sapiens
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P-PSDB; AAW01822.
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Matches 313; Conserv
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                                                                   357
                                  TCCCTGAACCTGAACTCTGTGACCGCCGCGGGACACGGCCGTGTATTACTGTGCCAGAGAT 300
                                                                                                      TGGGCCCAAATAGCTGGAACAA-------CGCTAGGCTTCTGGGGCCAGGGA 345
                                                                                                                                       cercrititicaerierregaareeriracaacaacreerregarereregeceeega 417
                                                                                                                                                                                                                                                                                                                                                                                                                                            Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
 238 TACAACCCCTCCAAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B cells, e.g. graft rejection or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= 16C10 heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                           Macaque primatized 16C10 heavy chain DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                            GTCCTGGTCACCGTCTCCTCA 366
                                                                                                                                                                                                              Greeregreacegrerere 438
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                                                                                                                                                                                                                                                                                                    BP.
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297
anti-idiotype reagents. MAD's are optionally combined with other proteins or small molecule immunosupressants. Blocking B7/CD28 interactions fuduces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunoglobulin G (IgG) responses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA sequence of a primatised form of the heavy chain of 16C10 antibody.
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                                                                                                                                                                                                                                                          DB 19; Length 1431;
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                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                               Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;
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                                                                                                                                                                                                                                                                                       Pred. No. 6.1e-61;
                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                          Score 256.2;
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                                                                                                                                                                                                                                                             70.0%;
                                                                                                                                                                                                                                                                                           82.28;
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Matches 313; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                idiopathic thrombocytopenia purpura, sistemic lupus, erythematoens, type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, infilammatory bile disease, allergy, multiple sclerosis or graft-ve-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or rejection of transplanted organ or tissue for treating proliferative airways disease, intestinal inflammations and allergies e.g. Crohn's disease and ulcerative colitis, food-related allergies e.g. Crohn's disease and ulcerative colitis, food-related allergies e.g. migraine, rhinitis and eczema, and other types of allergies right migraine, acid sequence encodes the heavy chain of 16c10, a primatised antibody used in the invention to induce apoptosis and inhibit production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCTGCGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGGCTGGATCCGCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACAACCCCTCCAGAGTCAAGTCACCATTTCAACAGACACGTCCAAGAACCAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGCCCGTGTATTACTGTGCCAGAGAT
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                                                                                                                                                    Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
                                                                                                                                                                                                                                                                           The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD86) for inducing the apoptosis of B7+ cells. The invention is useful for treating diseases such as B cell cancer, lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 24; Length 1431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 256.2; DB 2.
Pred. No. 6.1e-61;
0; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGGCCCAAATAGCTGGAACAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438
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                                                                                                                                                                                                                                              Example 8; Fig 5b; 89pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCCTGGTCACCGTCTCCTCA
                                                                     Brams
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22-MAY-2000; 2000US-0576424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 313; Conservative
                                  PHARM CORP
                                                                     Hanna N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interleukin-2 (IL-2)
                                                                                                       WPI; 2002-089895/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                         P-PSDB; AAU11646
                                  (IDEC-) IDEC
                                                                     Anderson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -
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RESULT 5 AAZ39331

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   caderecadricascadiceseccaseadrecreasecricesasaccreacerecret 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accrecacrercrescreere---crrcacracracracracaarregarcceccae 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 TGGGCCCAAATAGCTGGAA---CAACGCTAGGCTTCTGGGGCCCAGGGAGTCCTGGTCACC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides an antibody (Ab) comprising donor CDRs (complementarity determining regions) derived from a non-human antigenspecific donor antibody, and an acceptor framework from a non-human primate. The Abs are prepared by grafting CDRs from a non-human nutigenspecific donor antibody onto homologous Old World ape or monkey acceptor frameworks. The Abs have reduced immunogenicity and are better tolerated in humans (because of the close similarity between the human and primate process), but retain the full antigen-binding affinity of the donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibodies containing donor complementarity determining regions and non-human primate acceptor frameworks, having reduced immunogenicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                Complementarity determining region; antibody; primate; immuno; old World ape; Old World monkey; antigen-binding affinity; se
                                                                                                                                                             Nucleotide sequence of Cynomologous VH cDNA clone 2-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 423 BP; 76 A; 125 C; 122 G; 100 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 79; 123pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM CORP.
BP.
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  AAZ39331 standard; DNA; 423
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P-PSDB; AAY56663, AAY56728.
                                                                                                             (first entry)
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ses 307; Conserv
                                                                                                                                                                                                                                                                                                       Macaca cynomolgus
                                                                                                                                                                                                                                                                                                                                                         W09955369-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-APR-1998;
                                                                                                             15-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                            04-NOV-1999
                                                        AAZ39331;
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241 TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGAT 300
                                                                                                                                                                             TCCCCAGGGAAGGGACTGGAGTGGATGGGCTACATCTATGGCAGTGGTGGGGGCACCAAT 237
                                                                                                                                                                                                                                     301 TGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTC 360
                                                                                                                                                                                                                                                               DNA sequences (AAT62868-70) respectively code for the heavy chain regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S229P mutations. They can be used to provide novel monoclonal and chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in which the human 1gG4 Fc binding domain framework is combined with the antigen binding domains (see also AAW14922-23) of macaque anti-human CD4 monoclonal antibody E9.1. These antibodies show high affinity to human CD4, have little or no immunogenicity in humans and show reduced or absence of effector function. The
                                                                TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD4; monoclonal antibody; chimaeric antibody; recombinant antibody; cynomolgus monkey; autoimmune disease; rheumatoid arthritis; leukaemia; lymphoma; graft-versus-host disease; asthma; transplant rejection; HIV; therapy; CB9 gamma-4E; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gamma-4E and -4PE mutations confer activity enhanced stability and eliminate depleting activity. The antibodies can be used to treat autoimmune diseases such as rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric antibody comprising monkey variable domains and human constant domains - affects CD4-mediated immune functions, espuseful for treatment of autoimmune disease, e.g. rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Page 86-88; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT62869 standard; DNA; 1404 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human gamma-4E heavy chain DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reff ME;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-OCT-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IDEC-) IDEC PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanna N, Newman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-201913/18.
P-PSDB; AAW14926.
                                                                                                                                                                                                                                                                                                                                                                   TCCTCA 420
                                                                                                                                                                                                                                                                                                                           TCCTCA 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accrecerrererrendencecrererageagnagnaarragaaceregareeareeee 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 ACCTGCAGTGTCTCTGGTGGCTCCATCAGCGGTGACTATTATTGGTTCTGGATCCGCCAG 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequences (AAT62868-70) respectively code for the heavy chain regions of human gamma-4 (AAM14925), gamma-4 Ecarrying the L236E mutation (AAM14926) and gamma-4PE (AAM14927) carrying L236E and S2299 mutations. They can be used to provide novel monoclonal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CAGCTGCAGCTGCAGGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
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                                                                                                                                                                                                                                                                                                                                                  CD4; monoclonal antibody; chimaeric antibody; recombinant antibody; cyromolgue monkey; autoimmune disease; rheumatoid arthritis; leukaemia; lymphoma; graft-versus-host disease; asthma; transplant rejection; HIV; therapy; CE9 gamma 4; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric antibody comprising monkey variable domains and human constant domains - affects CD4-mediated immune functions, espuseful for treatment of autoimmune disease, e.g. rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be used to treat autoimmune diseases such as rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1404 BP; 312 A; 448 C; 377 G; 267 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Page 82-84; 155pp; English.
                                                                                                                                                                             AAT62868 standard; DNA; 1404 BP.
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                                                                                                                                                                                                                                                                                                       Human gamma-4 heavy chain DNA.
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                                                                    GTCTCTTCA 423
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P-PSDB; AAW14925.
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                                                    DB 18; Length 1404;
                                                                                                            Indels
Sequence 1404 BP; 313 A; 446 C; 379 G; 266 T; 0 other;
                                                                                                            65;
                                                                                  4e-58;
                                                                                                            0; Mismatches
                                                    67.2%; Score 246;
81.4%; Pred. No. 4
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DNA sequences (AAT62868-70) respectively code for the heavy chain regions of human gamma-4 (AAM14925), gamma-4E carrying the L236E mutation (AAM14926) and gamma-4FE (AAM14927) carrying the L236E mutations. They can be used to provide novel monoclonal and chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4FE, in which the human IgG4 Fc binding domain framework is combined with the antigen binding domains (see also AAM1492-23) of macaque anti-human CD4 monoclonal antibody E9.1. These antibodies show high affinity to human CD4, have little or no immunogenicity in humans and show reduced or absence of effector function. The gamma-4E and -4PE mutations confer activity enhanced stability and eliminate depleting activity. The antibodies can be used to treat cutoimmune diseases such as rheumatoid arthitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CAGCTGCAGCTGCAGGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC
                                                                                                                                         S229P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..747
/*t.gg= a
1..330
/*tag= b
/*tote= "light chain variable region coding sequence"
331..747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequence of antibody directed against K293 superantigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody; tumor; epithelial; colorectal; pancreatic; breast; lung; carcinoma; K293; immunostimulant; cytostatic; antisense therapy; v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Length 1404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1404 BP; 313 A; 447 C; 379 G; 265 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 246; DB 18
Pred. No. 4e-58;
0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.2%;
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PCR; amplify; clone; heavy; light; chain; variable; region; lambda; immortalised B-cell; vector; TCAB 6; human; 1gG1; constant; antigen; recombinant; antibody; chimpanzee; 1g; Ag; old world monkey; eczema; immunoglobulin; therapeutic; rheumatoid arthritis; ss.

coding sequence.

25-MAR-2003 08-JUN-1993 Anti-CD4 VH

(updated)
(first entry)

AAQ35903;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGCGCTGTCTCTGTGGCTCTGTCAGCAGTAGTAGTGGTGGACCTGGATCCGCCAGC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTGCGCTGTCTCTGGTTTCTCCCATCAGCAGTGGTTATGGCTGGAGCTGGATCCGTCAGT 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACCGTCCAAGAACCAGTTCT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAACCCGTCCCTCAAGAGTCGAGTCACCATTTCAAGAGACACGTCCAAGAACCAGTTCT 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCTGAACCTGAACTCTGTGACCGCCGCGGACACGCCGTGTATTACTGTGCCAGAGATT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCT 361

    - GATAGAGGCTGGCACGAÁTACTTCGACTTCTGGGGCCAGGGAGTCCTGGTCACCGTTT 742

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCCAGGGAAGGGACTGGAGTGGACGTATCTCTGGTAGTGGTGGGGCCCACCAACT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cccreaagcreaccrerereacececececacacececererarracrerereaeacar- 684
                                                                                                                                                                                                                                                                                             The invention provides a binding structure, such as an antibody, binding to tumor cells, especially epithelial tumor cells such as colorectal, pancreatic, breast or lung carcinoma cells. The binding structures, target structures to the binding structures or the substances, i.e. antisense oligonucleotides and ribozymes, are useful in the therapy and in vitro histopathological diagnosis and prognosis of human malignant disease. The present sequence represents the nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCA
                                                                                                                                                                                                              A binding structure, such as an antibody, binding to tumor cells, especially epithelial tumor cells such as colorectal, pancreatic, breast or lung carcinoma cells, useful in the therapy, diagnosis and prognosis of human malignant disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
 /*tag= c
/note= "heavy chain variable region coding sequence'
                                                                                                                                                      Tordsson MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 66.9%; Score 245; DB 22; Length 747; Best Local Similarity 83.3%; Pred. No. 6.4e-58; Matches 304; Conservative 0; Mismatches 55; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 747 BP; 149 A; 216 C; 211 G; 171 T; 0 other;
                                                                                                                                                      Ohlsson LG,
                                                                                                                                                                                                                                                                                                                                                                                 directed against K293 superantigen
                                                                                                                                                      Nilson BHK,
                                                                                                                                                                                                                                                                         Disclosure; Page 70-71; 73pp; English
                                                                                23-FEB-2001; 2001WO-SE00395.
                                                                                                       2000SE-0000597.
                                                                                                                                                      ЪЈ,
                                                                                                                               (ACTI-) ACTIVE BIOTECH AB
                                                                                                                                                      Brodin TN, Karlstroem
                                                                                                                                                                              WPI; 2001-565403/63.
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                                                                                                                                                                                         P-PSDB; AAB85908
                                                                                                       24-FEB-2000;
                                                          30-AUG-2001
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Recombinant antibodies including Old World monkey portion ar human portion - used for treatment of auto-immune diseases, infectious diseases, AIDS, tumours, diabetes, proliferative diseases, incestinal inflammations and allergies, etc.

Raab RW

WPI; 1993-058729/07

P-PSDB; AAR31948

92US-0856281.

23-MAR-1992;

DEC PHARM CORP Newman RA, Ra

(IDEC-) IDEC

Hanna N,

91US-0735064

24-JUL-1992; 25-JUL-1991;

WO9302108-A1

Simian

04-FEB-1993

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240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCTGCAGTGTCTCTGGTGGCTCCATCAGCGGTGACTATTATTGGTTCTGGATCCGCCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 CCCCCAGGGAAGGGACTGGAGTGGACGTATCTCTGGTAGTGGTGGGGCCACCAAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACAATCCCTCCTCAACAATCGAGTCTCCATTTCAATAGACACGTCCAAGAACCTCTTC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                          The sequences given in AAQ35903-04 encode the Simian anti CD4 VH and V-lambda sequences respectively. These sequences were derived using the primer sequences given in AAQ35901-02. The amplification products were sequentially cloned into the vector TCAE 6, which contains human 1gG1 and human lambda constant regions. The amplified sequences could be used in the production of a recombinant antibody, comprising a human, chimpanzee or old world monkey immunoglobulin (1g) constant region and an antigen (Ag) binding portion of an old world monkey ig varible region, where the old world monkeys may be the same or different. The recombinant antibody may be used as a therapeutic agent for the treatment of rheumatoid arthritis, eczema and immunological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.8%; Score 244.4; DB 14; Length 81.1%; Pred. No. 8.2e-58; cive 0; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                (Updated on 25-MAR-2003 to correct PN field.)
Disclosure; Page 53-54; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 297; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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AAQ35903 standard; DNA; 423 BP

RESULT 10 AAQ35903 ID AAQ3: XX ä

Gaps

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66; Indels

DB 18; Length 423;

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301 301 361

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418 361

> RESULT 11 AAT91564

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ACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
                                                                                                                                                                                                                                                                                                                    TACAACCCGTCCCTCAAGAGTCGAGTCATTTTCACAAGACCACGTCCAAGAACCAGTTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 TCCCTGAACCTGTGACCGCCGCGGGACACGGCCGTGTATTACTGTGCCAGAGAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 TGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGCCCAGGGAGTCCTGGTCACCGTC 360
                                                                                                                                                                                                                                                                                                                                                                                                 121 CCCCCAGGGAAGGGACTGGAGTGGACGTATCTCTGGTAGTGGTGGGGCCACCAAC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---ATATTGAAATATCTTCACTGGTTATTATACTGGGGCCAGGGAGTCCTGGTCACCGTC 417
                                                                                                                                                                     CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4..423
/trag= a
/transl_except= (pos:415..417, aa:Ser)
/product= "Variable heavy chain antigen binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-CD4 antibody, antigen-binding, treatment, chimeric; human; monkey, rheumatoid arthritis; psoriatic arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-CD4 antibody variable heavy (VH) region encoding DNA.
Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;
                                                     Query Match 66.8%; Score 244.4; DB 19
Best Local Similarity 81.1%; Pred. No. 8.2e-58;
Matches 297; Conservative 0; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric - Macaca cynomolgus.
Chimeric - Homo sapiens.
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91US-0735064.
92US-0856281.
92US-0912292.
95US-0379072.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 TCCTCA 366
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23-MAR-1992;
10-JUL-1992;
25-JAN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-CD4 cynomolgus monkey immunoglobulin heavy chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/product= Anti-CD4_VH_region
/note= "No stop codon_given"
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91US-0735064.
92US-0856281.
95US-0379072.
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Hanna N, Newman RA, Raab RW;

(IDEC-) IDEC PHARM CORP.

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07-JUN-1995;
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                                                                                                                                                                                          This DNA encodes the heavy chain variable region (VH) of the cynomolgus monkey anti-CD4 antibody. The antibody comprises antigen-binding sequences from an Old World monkey antibody and human constant domain sequences. The antibody specifically binds to CD4 and can be used in the treatment of rheumatoid or psoriatic arthritis.
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/note= "no stop codon given at the 3' end of sequence"
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                                                                                 Treatment of rheumatoid and psoriatic arthritis - comprises administration of chimeric human-monkey anti-CD4 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                    66; Indels
                                                                                                                                                                                                                                                                                                                                Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                         Score 244.4; DB 1
Pred. No. 8.2e-58;
                                                                                                                                                                                                                                                                                                                                                                      Query Match 66.8%; Score 244.4; Best Local Similarity 81.1%; Pred. No. 8.2e Matches 297; Conservative 0; Mismatches
                                                                                                                                                   Claim 2; Columns 35-36; 47pp; English
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81.1%; Pred. No. 8.2e-58;
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92US-0856281
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/*tag= }
61..420
/*tag= 0
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Best Local Similarity
Matches 297; Conserv
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121 CCCCCAGGGAAGGGACTGGAGTTGGACGTATCTCTGGTAGTGGTGGGGCCACCAAC 180
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                                                                                                                                 CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human diagnostic and therapeutic molecule; dithp; gene therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human diagnostic and therapeutic (dithp) cDNA sequence #37.
                               Pred. No. 8.2e-58;
0; Mismatches 66
   Score 244.4;
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99US-0156294.
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99US-0156624.
99US-0167410.
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99US-0167520.
99US-0167943.
99US-0167943.
99US-0168197.
   66.8%;
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Query Match
Best Local Similarity 81.13
Matches 297; Conservative
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24-NOV-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant chimeric antibodies comprising human, chimpanzee and Old World monkey portions, useful for treating e.g. cancer, eczema, leukemia, lymphoma, Hashimoto's thyroiditis, multiple sclerosis or male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Old world monkey; monkey; tumour; cancer; ds; immunoglobulin variable region; immunoglobulin variable region; autoimmunoglobulin variable region; autoimmune response; rheumatoid arthritis; eczema; lymphoma; immunomodulatory disease; leukaemia; Hashimoto's thyroiditis; autoimmune carditis; Addison's disease; type I-diabetes mellitus; multiple sclerosis; male infertility; autoimmune hemolytic anaemia; inflammatory bowel disease; Sjogren's syndrome; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                               cynomolgus monkey immunoglobulin heavy chain.
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                                                                                                                                                                                                              ABX76616 standard; DNA; 423 BP
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95US-0476237.
98US-0082472.
91US-0735064.
92US-0856281.
95US-0397072.
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P-PSDB; ABU56789.
                                          423
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                                      TCCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-1992;
17-APR-1995;
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30-NOV-1999;

9-NOV-1999 29-NOV-1999

lupus erythematosus. This is the amino acid sequence of a monkey immunoglobulin heavy variable chain polypeptide for creation of

Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;

recombinant antibody

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The present sequence for human diagnostic and therapeutic (dithp) cDNA sequence #37 is 1 of 71 (AAS03012-AAS03082) novel sequences described in the invention. The present sequence (Incyte ID No: 4442487dec) concodes an antigen recognition molecule. The dithp polymucleotides may be used to diagnose a condition disease or disorder associated with human molecules. They can be used to identify the presence of similar nucleic acids. Dithp polymucleotides may used to generate hybridisation probes for use in chromosomal mapping. Polypeptides (DITHP) encoded by cithp are used to screen for molecules which bind to them and modulate their activity. Dithp polymucleotides can be used for gene therapy of disorders such as severe combined immunodeficiency syndrome (SCID), cystic fibrosis, thalassemia, haemophilia resulting from Factor VIII or III proliferative disorders e.g. cancers, hypercholesterolaemia (FH), cell proliferative disorders e.g. cancers, neurodegenerative disorders, autoimmune/inflammatory disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurodegenerative disorders, autoimmune/inflammatory disorders,
infectious disorders and developmental disorders. The antibodies can be
                                                                                                                                                                                                                                                                                                                            Yap PE, Stockdreher TK;
                                                                                                                                                                                                              Banville SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel diagnostic and therapeutic polynucleotides, used in disease diagnosis and for gene therapy of conditions such as cancer and thalassemia
                                                                                                                                                                                                                                                                     Shah P, Cl
Panzer SR;
                                                                                                                                                                                                                               Russo FD, Spiro PA,
Cohen HJ, Rosen BH,
Yu JY, Greenawalt LB,
J, Chen W, Liu TF, Ya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used to analyse protein expression levels.
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                                  99US-0168432.
99US-0168468.
99US-0168599.
   99US-0168429
                                                                                                                                                                 (INCY-) INCYTE GENOMICS INC
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Bratcher SR, Dufour ob,
Hillman JL, Jones AL, Yu
                                                                                                                                                                                                                                   Lincoln SE,
Dufour GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-281607/29.
                                                                                                                                                                                                                                                                                                                                                                     Fong WT
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01-DEC-1999;
01-DEC-1999;
30-NOV-1999;
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Sequence 619 BP; 121 A; 192 C; 176 G; 130 T; 0 other;

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93 CAGGIGCAGCIGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTC 152
                                                                                                                                                                                    ACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
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                                              Gaps
                                            9
DB 22; Length 619;
Query Match 66.7%; Score 244.2; DB 22; Length Best Local Similarity 82.7%; Pred. No. 1e-57; Matches 305; Conservative 0; Mismatches 58; Indels
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Search completed: December 29, 2003, 16:25:37 Job time : 161.688 secs

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Sequence 65, Appl

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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NBW PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
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14: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
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                                          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Sequence 2, A Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 7, A Sequence 7, A Sequence 11, As Se US-09-019-441-2 5 US-10-103-686-2 US-10-124-807-11 US-10-124-807-11 US-10-291-532-11 US-10-291-532-11 US-10-291-532-11 US-10-131-38-6 US-09-905-243-4 US-10-211-357-7 US-10-211-357-11 US-10-211-357-11 US-10-211-357-11 US-10-211-357-11 US-10-211-357-11 US-10-850-165-15

Appl Appli

Sequence 44, Sequence 1,

US-10-211-357-1

244.4 242.8 241.4 245

25 Sequence 5., Appl.  29 Sequence 1, Appl.  29 Sequence 3, Appl.  29 Sequence 3, Appl.  20 Sequence 2, Appl.  20 Sequence 114467,  20 Sequence 114467,  20 Sequence 114467,  20 Sequence 114467,  2114 Sequence 114, Appl.  220 Sequence 59, Appl.  231 Sequence 59, Appl.  2401 Sequence 59, Appl.  252 Sequence 59, Appl.  262 Appl.  263 Sequence 59, Appl.  274 Sequence 1183, Appl.  275 Sequence 27, Appl.  276 Sequence 27, Appl.  277 Sequence 27, Appl.  278 Sequence 27, Appl.  279 Sequence 27, Appl.  270 Sequence 11, Appl.  271 Sequence 11, Appl.  272 Sequence 11, Appl.  273 Sequence 11, Appl.  28401 Sequence 15, Appl.  28401 Sequence 15, Appl.  28401 Sequence 15, Appl.  28401 Sequence 15, Appl.	23 MONOCLONAL EREOF AS THERAPEUT ATHIS, LLP Sion #1.30
US-109-97-55-65-65-95-96-95-96-96-96-96-96-96-96-96-96-96-96-96-96-	ALIGNMENTS  RESULT 1  US-09-019-441-2  Sequence 2, Application US/09019441  Sequence 2, Application No. US20030086921A1  GENERAL INFORMATION:  KLOETZER, William S.  NAKAMURA, Takehiko.  TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD  ANTIBODIES AND USE THAT BANTIBODIES AND USE THAT BODRES AND USE THAT BODRES AND USE THAT STREET:  CORRESPONDENCE ADDRESS:  ADDRESSE: BURNS, DOANE, SWECKER & MSTREET: P.O. Box 1404  CITY: Alexandria  STARET: VICTION AN ANTIBODIES AND USE THAT STREET: VICTION AND ANTIBODIES AND USE THAT STREET: P.O. Box 1404  COMPUTER: United States  ZIP: 22313-1404  COMPUTER: IBM PC compatible  COMPUTER: IBM PC compatible  COMPUTER: IBM PC compatible  SOFFWARE: PATENTIN PC-POS/MS-DOS  SOFFWARE: PATENTIN PC-POS/MS-DOS  SOFFWARE: PATENTIN AND ANTI-  APPLICATION NUMBER: US 08/803,085  FILING DATE: 20-FEB-1997  ATTORNEY/AGENT INFORMATION:  NAME: TESERNCE/DOCKET NUMBER: 012712-502  TELEFRAX: (703) 836-5620  INFORMATION FOR SEQ ID NO: 2:
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Best Local Similarity 100.
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TITLE OF INVENTION: TO H
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CORRESPONDENCE ADDRESS:
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NAKAMURA, Takehiko
TITLE OF INVENTION: GARMAL ANTI HUMAN CD23 MONOCLONAL
ANTIBODIES AND USE THEREOF AS THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAAGCCTTCGGAGACCCTG
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/103,686
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CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
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100.0%; Pred. No. 4.5e-104;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                           DOCATION: 58.7423
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-019-441-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/10103686 Publication No. US20030059424A1 GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
                                                                                                                                           MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                        LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                         NAME/KEY: mat_peptide
LOCATION: 58..423
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 1..423
                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      366; Conservative
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US-10-103-686-2
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Best Local S
Matches 366
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Anderson, Darrell R.
VENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
VENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
VENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
VENTION: IMMUNOSUPPRESANTS"
EQUENCES: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCCCAGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCGCACCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 366; DB 15;
Pred. No. 4.5e-104;
0; Mismatches 0;
              PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 836-6620
TELEFAX: (703) 836-620
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-103-686-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 11, Application US/09948429B; Patent No. US20020177689A1
GENERAL INFORMATION: GENERAL Anderson, Darrell R.
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                         LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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BURNS, DOANE, SWECKER & MATHIS

ADDRESSEE:

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Sequence 11, Application US/10124807
Publication No. US20030166207A1
GENERAL INFORMATION:
TITLE OF INVENTION: HONKEY MONCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: IMMUNOSUPPRESANTS"
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 13; Length 1431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 256.2; DB 1
Pred. No. 9.2e-70;
0; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: 09/383,916
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Teskin, Robin L. REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1431 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
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82.2%;
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Best Local Similarity 82.2
Matches 313; Conservative
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LOCATION:
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; LOCATION:
US-10-124-807-11
                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 ACCTGCGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGGCTGGATCCGCCAG 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 1431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 256.2; DB 10; Length Pred. No. 9.2e-70; 0; Mismatches 53; Indels
                                                                                                                                              COMPUTER: IBM PC COMPACATED COMPACATION SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGGCCCAAATAGCTGGAACAA-----
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                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFFCATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teakin, Robin L.
RECISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01271
TELECOMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-6020
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                     COUNTY
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
POTOMORTIPE: POTOMORTIBLE
PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not relevant
: 699 Prince Street
Alexandria
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82.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1431 base pairs
IYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 82.2
Matches 313; Conservative
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MOLECULE TYPE: peptide
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1..1431
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY:
; LOCATION:
US-09-948-429B-11
                                              STATE: V. COUNTRY:
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APPLICANT: Anderson, Darrell R.

IITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGGIIGCAGCIGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTC 117
298 TCCCTGAAGCTGAACTCTATGACCGCCGCGGACACGGCCGTGTATTACTGTGTGAGAGAT 357
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                                                                                                                  70.0%; Score 256.2; DB 14; Length 1431; 82.2%; Pred. No. 9.2e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street
CITY: Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                      346 GTCCTGGTCACCGTCTCTCA 366
                                                                                                                                                                                                                           GICCIGGICACGICICCICA 438
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/10124905; Publication No. US20020166136A1 GENERAL INFORMATION:
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                                                                   301 TGGGCCCAAATAGCTGGAACAA
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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EDNESS: not relevant
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 82.2
Matches 313; Conservative
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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FEATURE:
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UCATION:
US-10-124-905-11
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HANNA, NABIL
TITLE OF INVENTION: AMEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR INTITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
CURRENT REPERENCE: 03703/291872
CURRENT APPLICATION NUMBER: US/10/291,532
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 60/331,187
PRIOR FILING DATE: 2001-01-109
PRIOR APPLICATION NUMBER: 09/758,173
PRIOR FILING DATE: 2001-01-12
PRIOR PELING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 1999-08-26
PRIOR FILING DATE: 1990-08-26
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   TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGAT 300
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Pred. No. 9.2e-70;
0; Mismatches 53; Indels
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Publication No. US20030180290A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Matches 313; Conservative
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; LOCATION: (1)..(1428)
US-10-291-532-11
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                                                                                                                                                                                                                                                             Query Match 70.0%; Score 256.2; DB 14; Length 1431; Best Local Similarity 82.2%; Pred. No. 9.2e-70; Matches 313; Conservative 0; Mismatches 53; Indels 15;
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Sequence 40, Application US/09905243

Patent No. US2002006200941

GENERAL INFORMATION:
APPLICANT: Taylor, Alexander H

TITLE OF INVENTION: Monoclonal Antibodies with Reduced
TITLE OF INVENTION: Immunogenicity
FILE REFERENCE: P50770

CURRENT APPLICATION NUMBER: US/09/905,243

CURRENT FILING DATE: 1999-04-26

PRIOR APPLICATION UNMERE: 09/300,970

PRIOR FILING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 97

SEQ ID NOS: 97

LENGTH: 423
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83.2%; Pred. No. 4e-67;
iive 0; Mismatches 56;
                                              LOCATION: 1..1431
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346 GTCCTGGTCACCGTCTCCTCA, 366
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Best Local Similarity 83.2
Matches 307; Conservative
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US-09-905-243-40
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LOCATION: (1)
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INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7.1
AND B7.2 CO-STIMULATORY ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACAACCCCTCCTCAAGAGTCAAGTCACATTTCAACAGACACGTCCAAGAACCAGTTC 297
                                                                                                                                                                                                                     CCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTCTGGTAGTGGTGGGGCCACCAAC 180
                                                                                                                                                                                                                                                                                          TACAACCCGTCCCTCAAGAGTCGAGTCATTTCACAAGACACGTCCAAGAACCAGTTC 240
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                                                                                                 118 Accrecerererereseseres reaces and a Accres secres estas 
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STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
SOFTWARE: PatentIn Release #1.0, Version #1.30
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APPLICATION NUMBER: US/10/073,138
FILING DATE: 13-Feb-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/746,361
FILING DATE: 08-NOV-1996
FILING DATE: 07-JUN-1995
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NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-256
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Publication No. US20020187146A1
GENERAL INPORMATION:
APPLICANT: ANDERSON, Darrell R.
HANNA, Nabil
BRAMS, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GICCIGGICACCGICTCCICA 366
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MOLECULE TYPE: DNA (genomic)
FEATURE:
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STRANDEDNESS: single
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TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC 240
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                                                                                                                                                                                                                                                                                                                                         118 ACCTGCAGTGTCTCTGGTGGCTCCATCAGCGGTGACTATTATTGGTTCTGGATCCGCCAG 177
                                                                                                                                                                                                                                                                                                                                                                                      121 CCCCCAGGGAAGGGACTGGAGTTGGACGTATCTCTGGTAGTGGTGGGGCCACCAAC 180
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Reff, Mitchell B.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
Therapy
                                                                                                                                          Length 1404;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
COUNTRY: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: RIM PC Compatible
COMPUTER: PIN PC COMPATIBLE
COMPUTER: PIN PC COMPATIBLE
COMPUTER: PIN PC COMPATIBLE
COMPUTER: PIN PC COMPATIBLE
COMPATIBLE PATENTIN Release #1.0, Version #1.30
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                                                                                                                                                                                    92
                                                                                                                                      Score 246; DB 15;
Pred. No. 1.4e-66;
0; Mismatches 65;
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APPLICATION NUMBER: US 08/523,894 FILING DATE: 06-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/211,357
                                      NAME/KEY: mat peptide
LOCATION: 1..1404
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/10211357
Publication No. US20030077275A1
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
                                                                                                                                          Query Match 67.2%;
Best Local Similarity 81.4%;
Matches 298; Conservative (
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1..1404
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LOCATION:
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                     FEATURE
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                                                                                                      TACAACCCGTCCCTCAAGAGTCGAGTCATTTCACAAGACACGTCCAAGAACCAGTTC 240
                                                                                                                                 TCCCTGAACCTGAACTCTGTGACCGCGGGGGCACGGCCGTGTATTACTGTGCCAGAGAT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Newman, Roland A.
Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
Therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/612,914A
FILING DATE: 10-010-2000
APPLICATION NUMBER: US 08/523,894
FILING DATE: 06-5EP-1995
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, NOBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/211,357
FILING DATE: 05-Aug-2002
CLASSIFICATION: <UNKNOWD>
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TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/10211357
Publication No. US20030077275A1
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic) POSITION IN GENOME:
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STRANDEDNESS: single
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NAME/KEY:
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US-10-211-357-7
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                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 246; DB 15;
Pred. No. 1.4e-66;
0; Mismatches 65;
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APPLICATION NUMBER: US/09/612,914A
FILING DATE: 10-JU1-2000
APPLICATION NUMBER: US 08/523,894
FILING DATE: 06-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
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APPLICATION NUMBER: US/10/211,357
FILING DATE: 05-Aug-2002
CLASSIFICATION: <university control of the control of th
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TELEPHONE: 703-836-6620
                                                                                                                   ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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INFORMATION FOR SEQ ID NO: 11:
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ilarity 81.4%;
Conservative
CITY: Alexandria
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Best Local Similarity
Matches 298; Conservat
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHROMOSOME/SEGMENT: heavy chain gamma 4 with the E mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hanna, Nabil
APPLICANT: Hanna, Nabil
Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
RADBRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>ښ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 15; Length 1404;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 246; DB 15;
Pred. No. 1.4e-66;
                                                                              REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.2%; sc. No. 1.81.4%; Pred. No. 1.00 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: mat peptide
LOCATION: 1..1404
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/10211357
Publication No. US20030077275A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
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Best Local Similarity
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US-10-211-357-11
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61 ACCTGCGCTGTCTGGTGGCTCTGTCAGCAGTAATAACTGGTGGACCTGGATCCGCCAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 CCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCCACCAAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 TACAACCCGTCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTTTACTGTGCCAGAGAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 caegrecaecrecaegaegecegeccaegaeregreaaecerregaegaeaecerecere 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 Tacaarcecreereaacaarceaerereearricaaraeaeacaeereeaaaaaeeeeeree
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GENERAL INFORMATION:
APPLICANT: NEWMAN, ROLAND A.
APPLICANT: NEWMAN, ROLAND A.
APPLICANT: HANNA, NABIL.
APPLICANT: RAAB, RONALD W.
TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
FILE REPREBENCE: 037003-0280614
CURRENT APPLICATION NUMBER: 08/09/850,165
CURRENT FILING DATE: 1996-05-08
PRIOR PELICATION NUMBER: 08/476,237
PRIOR APPLICATION NUMBER: 08/476,237
PRIOR PELICANION NUMBER: 08/397,072
PRIOR PELICATION NUMBER: 09/912,292
PRIOR PELICATION NUMBER: 07/912,292
PRIOR APPLICATION NUMBER: 07/912,292
PRIOR APPLICATION NUMBER: 07/912,292
PRIOR APPLICATION NUMBER: 07/912,292
PRIOR PELING DATE: 1992-03-23
PRIOR PELING DATE: 1992-03-23
PRIOR FILING DATE: 1992-07-25
NUMBER OF SEQ ID NOS: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 423;
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Pred. No. 3.5e-66;
0; Mismatches 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 81.1%;
Matches 297; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: (4)..(420)
US-09-850-165-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 15
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                                                                                                                                                                                                                                   GENERAL INCREMINION. Thomas N.

APPLICANT: Brodin, Thomas N.

APPLICANT: Brodin, Thomas N.

APPLICANT: Nilson, Bo. H.K.

APPLICANT: Oldsson, Bo. H.K.

APPLICANT: Ordsson, W. Jesper

TITLE OF INVENTION: No. US20030176661Alel Antibody with Specificity for Colon Cancer;

FILLE REFERENCE: 003300-984

CURRENT APPLICATION NUMBER: US/10/182,132

CURRENT FILING DATE: 2002-09-05

PRIOR APPLICATION NUMBER: SC 0000597-5

PRIOR FILING DATE: 2000-02-24

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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COGATION: (1)..(747)
OTHER INFORMATION: K293 variable region (scFv); PRT (aa)-sequence OTHER INFORMATION: (1-110), mod Huston (111-129), Vh (130-249)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-09-850-165-15
; Sequence 15, Application US/09850165
                                                                                                                                                                         ; Sequence 1, Application US/10182132 ; Publication No. US20030176661A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Macaca fascicularis
                366
                                                         415 rccrch 420
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Search completed: December 30, 2003, 03:42:10 Job time : 529.775 secs
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NAME/KEY:
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Reff, Mitchell B.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human Therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
          TITLE OF INVENTION: Monoclonal Antibodies with Reduced
TITLE OF INVENTION: Immunogenicity
FILE REPERENCE: P50770
CURRENT APPLICATION NUMBER: US/09/905,243
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/300,970
PRIOR PILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 97
SEQTWARE: FastSEQ for Windows Version 3.0
LENGTH: 420
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                                                                                                                                                                                                                                                                                                                                                                            Score 242.8; DB 9;
Pred. No. 1.1e-65;
0; Mismatches 67;
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COMPUTER: IBM PC compatible
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CITY: Alexandria
STATE: VA
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ADDRESSEE: BURNS, DOANE,
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Publication No. US20030077275A1
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
Taylor, Alexander H
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.9%;
Matches 296; Conservative
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                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Macaca cynomolgus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 22314-3187
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US-09-905-243-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHROMOSOME/SEGMENT: light variable domain of CE9.1
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Version #1.30
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Pred. No. 3e-65;
0; Mismatches 66;
                                                                 FILING DATE: 05-Aug-2002

CLASSIFICATION: cunknown>
PRIOR APPLICATION NUMBER: US/09/612,914A

APPLICATION NUMBER: US/09/612,914A

FILING DATE: 10-Jul-2000

APPLICATION NUMBER: US 08/523,894

FILING DATE: 06-SEP-1955

ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-165

TELEPHONE: 703-836-6620

TELEPHONE: 703-836-620

TELEPHONE: 703-836-2021

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 base pairs
SOFTWARE: Patentin Release #1.0, 'CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/211,357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 61..420
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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Best Local Similarity 81.0%;
Matches 294; Conservative
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Tue Dec 30 06:26:56 2003
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Sequence 61, Appl
Sequence 4, Appli
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Sequence 59, Appl
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Sequence 11,
Sequence 7,
Sequence 9,
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Sequence 19,
Sequence 19,
Sequence 15,
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Sequence 107
Sequence 1,
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-523-894-9
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US-08-476-231-11
US-08-476-237-15
US-08-476-237-15
US-08-476-237-107
US-08-478-039-107
US-08-56-3494-1
US-08-589-9
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US-09-014-880-9
US-09-014-803-9
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US-08-545-809A-59
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0., Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length
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		US/08803085  tchell E. , William S. , Takehiko. GAMMA-1 ANTI-HI ANTIBODIES AND 35 SS: DOANE, SWECKER 1404  RM: RM: RM: Tates RM: Tates RM: RM: RELease #1.0, DATA: 1 Release #1.0, DATA: 1 US/08/803,08 EB-1997 L4 MATION: R1 35,030 R1 35,030 R1 35,030 R1 10,03 R1 35,030 R1 10,03 R1 10	
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6 4 6 4 6 4 6 4 6 4 6 4 6 4 6 4 6 4 6 4		ULT 1  08-803-085-2  equence 2, Application US/08803085  equence 1, Application US/08803085  extent No. 6011138  APPLICANT: REFF, Mitchell E. APPLICANT: RACETZER, William S. APPLICANT: NAKAWUA, Takehiko TITLE OF INVENTION: ANTIBODIES AND UNUBER OF SEQUENCES: 35  CORRESPONDENCE ADDRESS: ADDRESSER: BURNS, DOANE, SWECKER & STREET: P.O. Box 1404  CITY: Alexandria STARET: P.O. Box 1404  CITY: Alexandria STARET: P.O. Box 1404  CITY: Alexandria STARET: P.O. Box 1404  COUNTER EADABLE FORM: MEDIUM TYPE: FLOPPY disk COMPUTER READABLE FORM: MEDIUM TYPE: PLOPPY disk COMPUTER READABLE FORM: MEDIUM TYPE: PLOPPY disk COMPUTER READABLE FORM: APPLICATION NUMBER: US/08/891085  FILING DATE: 20-FEB-1997  CLASSIFICATION: A24  ATTORRENT APPLICATION HORBER: 012712-33  TELECOMUNICATION INPORMATION: TYPE: nucleic acid STRANDEDNESS: single TYPE: andle	23 peptide 423
N. W. O. W. G. G. A. W. W. W. W. W. W. G. G. G. W. W. W. W. W. W. G. G. G. G. W. W. W. W. W. G. G. G. G. G. W.		Cation:  If No. 1999  If No. 19	142 mat_p
		2, Application 2, Application 5, 6011138 CANT: REFF, Mi CANT: REFF, Mi CANT: REFF, Mi CANT: NAKAMURE OF INVENTION: OF INVENTION: OF INVENTION: OF INVENTION: A OF SEQUENCES; SPONDENCE ADDRE RESSEE: BURNS, RESSEE: BURNS, RESSEE: BURNS, TER READABLE FOR TER TERY: United & TER READABLE FOR TERY: THE NEADABLE FOR TERY: THE ASSENTINE OF SECUENCE TO NOWER TERY: THON FOR SEQ. INCE CALARDENCES: SIT NOWER TERY: THON FOR SEQ. INCE CALARDENCES: SIT NOWER TERY: THE TYPE: DNA	 D⊣ ছv
777 4 4 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6		1. Age of the property of the	
2009 2009 2009 2009 2009 2009 2009 2009		TITE OF 11138  PEREAL INFORMATION: APPLICANT: REFF, MIT APPLICANT: REFF, MIT APPLICANT: RAPETZER, APPLICANT: RAPETZER, APPLICANT: RAPETZER, APPLICANT: RAPETZER, APPLICANT: RAPETZER, APPLICANT: RAPETZER, TITLE OF INVENTION: APPLICATION: APPLICATION OF SECULATION OF SYSTEM: SOFTWARE: PROPRIMER: FILING DATE: 20-FE CLASSIFICATION NUMBER: FILING DATE: 20-FE CLASSIFICATION NUMBER: TELEPAN: 7031 836 NAME: TESERENCE/DOCKET NU TELEPAN: (703) 836 TELEPAN: (703) 836 TELEPAN: ASS DID TYPE: NUCLEIC SECULATION NUMBER: TELEPAN: (703) 836 TELEPAN: 123 DASS DID TYPE: NUCLEIC SECULATION OF SEQUID TYPE: NUCLEIC SECULATION OF SECULATION OF SEQUIP TYPE: NUCLEIC SECULATION OF SECU	NAME/KEY LOCATION FEATURE: NAME/KEY LOCATION
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		RESULT 1  US-08-803-085-2  Sequence 2, Application US/08803085  Patent No. 6011138  APPLICANT: REFF, Mitchell E. APPLICANT: MOFOTZER, William S. APPLICANT: MAKAMURA, Takehiko TITLE OF INVENTION: GAMA-1 ANTI STREET: P.O. BOX 1404 CORRESPONDENCE ADDRESS: ADDRESSEE: BURNS, DOANE, SWECH STREET: P.O. BOX 1404 CITY: Alexandria STATE: VIEGINA COUNTRY: United States ZIP: 22313-1404 COUNTRY: United States ZIP: 22313-1404 COMPUTER: EADABLE PORM: MEDIUM TYPE: FLOPS/MS-D SOFTWARE: Patent In Release #1. CURRENT APPLICATION DATA: MEDIUM TYPE: Patent IN PC-DOS/MS-D SOFTWARE: Patent IN RELEASE #1. CURRENT APPLICATION NUMBER: US/08/803, FILING DATE: 20-FEB-1997 CLASSIFICATION NUMBER: 35,030 FEFFERENCE/DOCKET NUMBER: 35,030 FEFFERENCE/DOCKET NUMBER: 35,030 TELEFONMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMUNICATION INFORMATION: TELECOMMUNICATION INFOR	; ; ; ; US-08-8
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100.0%; Score 366; DB 3; Length 423;

Query Match

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APPLICATION NUMBER:
FILING DATE: 07-JUI
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Best Local Similarity
Matches 313; Conserv
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                                                           LOCATION:
FEATURE:
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; LOCATION:
US-08-487-550-11
                               NAME/KEY:
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"MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
IMMUNOSUPPRESANTS"
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MEDIUM TYPE: Floppy disk
COMPUTER: Compatible
COMPUTER: Patent PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
           Pred. No. 3.5e-101;
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CITY: Alexandria
STATE: VA
100.0%; Pred. ...
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NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
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TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
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SEQUENCE CHARACTERISTICS:
           Best Local Similarity 100.
Matches 366; Conservative
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TELEPHONE: 703-836-2021
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US-08-487-550-11
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TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMBA B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
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                                                                                          1 CAGCTGCAGCTGCAGGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
                                              Gape
                                              15;
Length 1431;
                                            Indels
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APPLICATION NUMBER: US/09/526,098
                                                 53;
DB 3;
Score 256.2; DB :
Pred. No. 6.7e-68
                                            0; Mismatches
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07-JUN-1995
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; Sequence 11, Application US/09526098

; Patent No. 6492134

; GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
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ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
TOWNTER: IBM PC COMPATIBLE
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Query Match 67.2%; Score 246; DB 3; Best Local Similarity 81.4%; Pred. No. 7.9e-65; Matches 298; Conservative 0; Mismatches 65
                                                                                                                                    ATTORNEY FACENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECHONE: 703-836-6620
TELEPHONE: 703-836-2021
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                 LENGTH: 1404 base pairs
                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
COMPUTER READABLE FORM:
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LOCATION:
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US-08-523-894-7
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Sequence 7, Application US/08523894
Patent No. 6136310.
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Therapy
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                      Length 1431;
                                                                                                                                                                                                                                                                                                                                                                                                                        53; Indels
                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
                                                                                                                                                                                                                                                                                                                                                                                      70.0%; Score 256.2; DB 4
82.2%; Pred. No. 6.7e-68;
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STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        418 GTCCTGGTCACCGTCTCCTCA 438
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              NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01271
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-620
INFORMATION FOR SEQ 1D NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1431 base pairs
                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 313; Conservative
                                                                                                                                                                                                                                                                                                                 mat_peptide
                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
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22314-3187
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                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                   , LOCATION:
US-09-526-098-11
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61 ACCTGCGCTGTCTCTGGTGGCTCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65; Indels
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PLLING DATE: 06-SEP-1995
CLASSIPICATION: 424
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61 ACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
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                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Hanna, Roland A.
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 246, DB 3; Length 1404;
Pred. No. 7.9e-65;
0; Mismatches 65; Indels
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POSITION IN CENOME:
CHROMOSOME/SEGMENT: heavy chain gamma 4 with the P and E
CHROMOSOME/SEGMENT: mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/08523894
Patent No. 6136310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Best Local Similarity 81.4%;
Matches 298; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1..1404
                                           361 TCCTCA 366
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LOCATION:
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LOCATION:
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APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHROMOSOME/SEGMENT: heavy chain gamma 4 with the E mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 65; Indels
                                                                                                                                                                                              COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
TELEFAX: 703-836-6620
TELEFAX: 703-836-2021
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Pred. No. 7.9e-65;
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MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.2%;
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 81.4<sup>1</sup>
Matches 298; Conservative
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STRANDEDNESS: singl
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LOCATION:
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LOCATION:
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Indels

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240 240 300 300

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121 CCCCCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAAC 180
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                                                                                                                        61 caderecaderecadadecededecedadacrecradadecriregadacecererere 120
                                                                                                                                                                         61 ACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG
                                                                                                                                                                                                                        121 Accriscagistricrostoscriccarcascesicacuarraristricrostoscos
                                                                                                                                                                                                                                                                                                    TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---ATATTGAAATATCTTCACTGGTTATTATACTGGGGCCAGGGAGTCCTGGTCACCGTC
                                                                         CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19, Application US/08481869
Patent No. 5693780
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: NEWMAN, Nabil
APPLICANT: RAAB, Ronald W.
TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STRET: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,869
81.1%; Pred. No. 1.6e-64;
tive 0; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/379,072A
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/379,0728
FILING DATE: 25-JAN-1995
APPLICATION NUMBER: US 07/912,292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Rea, Teresa Stane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
Best Local Similarity 81.1
Matches 297; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCTCA 423
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                                                                                                   181 TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC 240
                                                                                                                                  TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGAT 300
                                                                                                                                                                                                                                                                                                    301 TGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTC 360
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                                                 178 TCCCCAGGGAAGGGACTGGAGTGGATCGGCTACATCTATGGCAGTGGTGGGGGCACCAAT 237
                                                                                                                                                                                                                                                     298 recergaaacrdaggrerdrgaecececececececererarracrdreceagraar 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: NEWMAN, Roland A.
APPLICANT: HANNA, Nabil
APPLICANT: HANNA, Nabil
APPLICANT: RAAB, Ronald W.
TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burne, Doane, Swecker & Mathis
STREET: P.O. BOX 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,072A
FILING DATE: 25-43N-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 13-MAR-1992
PRIOR APPLICATION NUMBER: US 07/735,064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0. V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/08379072A Patent No. 5658570 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: 8-63. Teresa Stanek
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 423 base pairs
TYPE: nucleic acid
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-UTL-1991
ATTORNEY AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-133
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION S186-620
TELEFANCE (703) 836-2021
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 TCCTCA 366
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US-08-478-039-107
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Patent No. 575696

GENERAL INFORMATION

APPLICANT: NEWMAN, Roland A.

APPLICANT: RAAB, Ronald W.

TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY.

NUMBER OF SEQUENCES: 18.

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: P.O. BOX 1404

COUNTRY: United States

COUNTRY: United States

STATE: Virginal

COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PR-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 66.8%; Score 244.4; DB 1
Best Local Similarity 81.1%; Pred. No. 1.6e-64;
Matches 297; Conservative 0; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/476,237
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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APPLICATION NUMBER: US 07/856,281
                             | TELEPHONE: (703) 836-6620
| TELEPHONE: (703) 836-2021
| INFORMATION FOR SEQ ID NO: 19:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 423 base pairs
| TYPE: nucleic acid
| STRANDEDNESS: single
| TOPOLOGY: linear
| MOLECULE TYPE: DNA (genomic)
| US-08-481-869-19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 TCCTCA 366
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US-08-476-237-15
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121 CCCCCAGGGAAGGGACTGGAGTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAAC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 TGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 ---ATATTGAAATATCTTCACTGGTATTATACTGGGGCCAGGGAGTCCTGGTCACGTC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 TACAATCCCTCCTCAACAATCGAGTCTCCATTTCAATAGACACGTCCAAGAACCTCTTC 300
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                                                                                                                                                                                                                                                    61 ACCTGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC
                                                                                                                             1 CAGCTGCAGCTGCAGGAGTCGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC
                                                                  Gaps
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Patent No. 5681722
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
ITILE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
   Length 423;
                                                                  Indels
   DB 1;
                                                                  99
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CITY: Alexandria
STATE: VA
COUNTY: USA
ZIP: 22313-1404
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
Query Match 66.8%; Score 244.4; DB 1
Best Local Similarity 81.1%; Pred. No. 1.6e-64;
Matches 297; Conservative 0; Mismatches 66
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418 TCC 420

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PatentIn Release #1.0, Version #1.30

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1 CAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTC 60
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                                                                                                                                                                                                                                        APPLICANT: Newman, Roland A.
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
ITILE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,349A FILING DATE: 07-JUN-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 241.4; DB 1;
Pred. No. 1.3e-63;
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Best Local Similarity 81.0%; Pred. No. 1.3e-
Matches 294; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
RHICR APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          012712-161
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APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
FILING APPLICATION DATA:
                                                                                                                                                    Sequence 107, Application US/08476349A
Patent No. 5750105
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POSITION IN GENOME:
CHROMOSOME/SEGMENT: Anti-CD4 VH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: FESKIN ESG., ROBIN L. REGISTRATION NUMBER: 35,030 REFERENCE/DOCKET NUMBER: 01 TELECOMMUNICATION INFORMATION: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
BDNESS: not relevant
GY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420 base pairs
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LOCATION: 61..420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4..420
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                                                                                                                                     JS-08-476-349A-107
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: TESKIN ESG., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
RELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEPHONE: 703-836-2021
INFORMATION FOR SEQ ID NO: 107: SEQUENCE CHARACTERISTICS:
LENGTH: 420 base pairs
TYPE: nucleic acid
                                                                                                                        CLASSIFICATION: 435
CLASSIFICATION: 435
REACR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
REACR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
REACR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
REACR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
SOFTWARE: PRICEIL DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,039
FILING DATE: 07-JUN-1995
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61..420
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LOCATION:
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; LOCATION:
US-08-478-039-107
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CAGGTGCAGCTGCAGGAGGGGGCCCAGGACTGAAGCCTTCGGAGACCCTGTCCTT 120
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TITLE OF INVENTION: Specifically Binding to Surface Antigen of
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                          ..
::
                                                                                                                                                                                  Length 420;
                                                                                                                                                                                                                          Indels
                                                                                                                                                                           Score 241.4; DB 3;
Pred. No. 1.3e-63;
0; Mismatches 66;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
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STREET: 805 Fifteenth Street, N.W., #700
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
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CLASSIPPICATION: 424
PRICH APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
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APPLICANT: NO. 5767246ihiko ITO
APPLICANT: Kazuhiro NAGAIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/08360125 Patent No. 5767246
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81.0%;
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Matches 294; Conservative
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61..420
                                          4..420
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                       NAME/KEY:
LOCATION:
FEATURE:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 ---ATATIGAAATATCITCACTGTIAITATATAGGGGCCAGGAGTCCTGGTCACCGTC 417
                                                                      ACCTGCGCTGTCTCTGGTGGCTCTCTCTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAG 120
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                                                                                                                                                               CCCCCAGGGAAGGGACTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAAC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Newman, Roland A.
APPLICANT: Neff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS
STREET: Alexandria
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POSITION IN GENOME:
CHROMOSOME/SEGMENT: light variable domain of CE9.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTER: VA

COUNTER: VA

COUNTER: 184

MEDIUM TYPE: Floppy disk

COMPUTER: ElAPPE Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/523,894

FILING DATE: 06-58P-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-165

TELEPHON: 703-836-2021

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTER:STICS:

LENGTH: 420 base pairs

TYPE: MINCHEDENCES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-523-894-1
; Sequence 1, Application US/08523894
; Patent No. 6136310
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MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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Sequence 9, Application US/08450578

Patent No. 5837845

GENERAL INFORMATION:
APPLICANT: Salvo HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Voko HIRAKAWA
APPLICANT: Voko HIRAKAWA
APPLICANT: Wo S37845ihiko ITO
APPLICANT: Wo S37845ihiko ITO
APPLICANT: WO SGATIAKI MONOCIONAI Antibody
ITTLE OF INVENTION: Human Monocional Antibody
ITTLE OF INVENTION: Geall Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                        178 TACTACAACCCGTCCCTCAAGAGTCGGAGTCACCATATCCGTAGACACGTCCAAGAACCAG 237
                                                                                                                      298 degadetraceseserractractracestracesteries descendes de consequence 357
178 AACTACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAG 237
                                                                                         238 TICTCCCTGAACCTGAACTCTGTGACCGCGGGGCGACACGGCCGTGTATTACTGTGCCAGA 297
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578
FILING DATE: MSY 25, 1995
CLASSIPICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. CHEEK, Jr.
REGISTATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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ORIGINAL SOURCE
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US-08-450-578-9
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65.0%; Score 237.8; DB 1; Length 3
Best Local Similarity 81.6%; Pred. No. 1.5e-62;
Matches 301; Conservative 0; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAPLOTYPE:
TISSUE TYPE:
TESTE TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                         NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEPHONE:
  FILING DATE: June 29, 1992 APPLICATION NUMBER:
                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TOPOLOGY: 1inear
MOLECULE TYPE: CDNA
HYPOTHETICAL:
                                                              ATTORNEY/AGENT INFORMATION:
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NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
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POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
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IMMEDIATE SOURCE:
LIBRARY:
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FRAGMENT TYPE:
ORIGINAL SOURCE:
                                             FILING DATE:
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VOLUME:
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APPLICANT: HIRAKAMA, YOKO
APPLICANT: HIRAKAMA, YOKO
APPLICANT: HIRAKAMA, YOKO
APPLICANT: NACAIKE, Kazuhiro
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
TITLE OF INVENTION: HUMBER: US/09/017,628
CURRENT APPLICATION NUMBER: US/09/017,628
CURRENT APPLICATION NUMBER: US/09/017,628
CURRENT APPLICATION NUMBER: US/360,125
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
LENGTH: 366
TAGAWA, Toshiaki
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                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Unknown
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       INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HARLOTYPE:
TISSUE TYPE:
CELL TYPE:
Hybridoma producing human antibody 1-3-1
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DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
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PEATURE:
NAME/KEY:
LOCATION:
LOCATION:
OTHER INFORMATION:
AUTHORS:
TITLE:
COURNAL:
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Best Local Similarity 81.67
Matches 301; Conservative
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IMMEDIATE SOURCE:
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POSITION IN GENOME:
CHROMOSOME/SEGMENT:
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RESULT 15
US-09-017-628-9
; Sequence 9, Application US/09017628
; Patent No. 5990287
; GENERAL INFORMATION:
; APPLICANT: HOSOKAWA, Saiko

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118 CAGCCCCCAGGGAAGGGACTGGAGTTGGACGTATCTCTGGTAGTGGTGGGGGCCACC 177
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                                                                                                     Query Match
65.0%; Score 237.8; DB 2; Length 366;
Best Local Similarity 81.6%; Pred. No. 1.5e-62;
Matches 301; Conservative 0; Mismatches 62; Indels 6
FEATURE:
, OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
US-09-017-628-9
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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	Search time 1466.44 Seconds (without alignments) 8875.644 Million cell updates/sec	CACCGICTCCTCA 354
sw model	December 29, 2003, 16:08:50 ; Search time 1466.44 Seconds (without alignments) 9875.644 Million cell updates/	US-09-019-441-4_COPY_58_411 354 1 GAGGTGCAGCTGGTGGAGTCTCCTGGTCACGTCTCCTCA 354
OM nucleic - nucleic search, using sw model	December 29, 2003,	US-09-019-441-4_COPY_58_411 354 1 GAGGTGCAGCTGGTGGAGTC
OM nucleic - nu	Run on:	Title: Perfect score: Sequence:

5777422 2888711 segs, 20454813386 residues Total number of hits satisfying chosen parameters: Scoring table: IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

			3920 Macaca	919 Macaca	3918	5355 Papio	5540 Human	1918	21 Macaca	5119 Homo sa	1780 Method f	7727 High	3673 Homo	1 Human i	3 Homo E	94 Human x	3923 Mace	11 Homo s	15 Homo		HOMO 8	Homo		Sequen	868 Method	luman Ig	Homo	Homo	ото вар	Maca	116	Homo	. H.sapien	H.sapien	œ	79 Method	57726 High	13 Human (f	150 Human i	363 Ното ва	398 Ното sap	716 Homo sapi	714 Homo sap	15107 Homo	982 Homo s	972 H.sapien	
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## ALIGNMENTS

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			Method for integrating genes at specific sites in mammalian cells	via homologous recombination and vectors for accomplishing the			BD075127.1 GI:22620730	221-A/3.	ad.	ğ	åď.	L to 19040)	Reff, M.E., Barnett, R.S. and Mclachlan, K.R.	Method for integrating genes at specific sites in mammalian cells	
		BD075127	Method for	via homolog	same.	BD075127	BD075127.1	JP 2001516221-A/3.	unidentified	unidentified	unclassified.	1 (bases 1 to 19040)	Reff, M.E.,	Method for	
RESOLT 1	BD075127	rocns	DEFINITION			ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM		REFERENCE	AUTHORS	TITLE	

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Germline repertoire of the immunoglobulin V(H)3 family in rhesus
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                                                               10912503
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                                                                                                                                                                                       source
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AUTHORS
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AF173919
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                                 JOURNAL
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   TITLE
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                                                           PF 09-MRA-1998 UP 1998540539
PR 14-MAR-1997 US 08/81986,13-FEB-1998 US 09/023715 PI
MITCHELL E REFF.RICHARD SPENCE BARNETT, KAREN RETTA MCLACHLAN PC
C12N15/90,C12N15/85,C12Q1/68,C12N5/10,C12N9/12,C12N15/13, PC
C07K16/28,
C C12N15/12,C07K14/705,G01N33/53,C12N15/62,C07K19/00 CC
Strandedness: Single;
C Topology: Linear;
C Method for integrating genes at specific sites in mammalian
CC Method for integrating genes at specific sites in mammalian
CC homologous recombination
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(Cranopithecinae, Macaca.

Helmuth, E.P., Letvin, N.L. and Margolin, D.H.
   via homologous recombination and vectors for accomplishing the Patent: JP 2001516221-A 3 25-SEP-2001;
IDEC PHARMACEUTICALS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTTACTGTGCGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9493 GAGGTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC
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Macaca mulatta immunoglobulin heavy chain variable segment
precursor (IGHV) gene, partial cds.
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/organism='Unidentified'
Location/Qualifiers
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                                                                                                                                                                                                                                                                               Location/Qualifiers
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Pred. No. 1e-81;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                             l. .19040
/organism="unidentified"
                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/db_xref="taxon:32644"
4976 c 4835 g 452
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                                                Unidentified
JP 2001516221-A/3
25-SEP-2001
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                                                                                                                                                                                                                                                                 same
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Best Local Similarity
Matches 351; Conserv
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AF173920
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REFERENCE AUTHORS

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/procesin id="AAF89376.1"
/db_xref="G1:9587773"
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/translation="MERGLSWVFLVALLKGVQCEVQLVESGGGLAKPGGSLRLSCAAS
/Frinslation="MERGRGLEWVSRISNGGGSTWYADSVKGRFTISRENAKNTLYLQM
NSLRAEDTAVYYCAKDTV"
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Macaca mulatta immunoglobulin heavy chain variable segment
precursor (IGHV) gene, partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394
                                                                                                 Margolin, D.H.
Direct Submission
Submitted (02-AUG-1999) Viral Pathogenesis Division, Beth Israel
Deaconess Medical Center, Research East 113, PO Box 15732, Boston,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/product="immunoglobulin heavy chain variable segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                /gene="IGHV"
/note="similar to human immunoglobulin heavy chain
variable segments of the VH3 family; synonyms: IgVH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function="putative recombinant recognition sequence (heptamer)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                463;
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Pred. No. 6.1e-59;
); Mismatches 13;
Immunogenetics 51 (7), 519-527 (2000)
20367631
                                                                                                                                                                                                                                  1. .463
/organism="Macaca mulatta"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="IGHV"
                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/db_xref="taxon:9544"
                                                                                                                                                                                                                                                                                                                  /tissue_type="kidney"
/germline
                                                                                                                                                                                                          Location/Qualifiers
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Best Local Similarity 93.6%;
Matches 279; Conservative
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/gene="IGHV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         precursor"
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                                                                               2 (bases 1 to 463)
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/db_xref="G1:9587769"
ftranslation="MBFGLSWVFLVALLKGVQCEVQLVESGGGLAKPGGSLRLSCAAS
ftranslation="MBFGKGLEWVSRISNGGGSTWYADSVKGRFTISRENAKNTLYLQM
DSLRAEDTAVYYCARDTV"
                                                                                    PRI 31-JUL-2000
segment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-AUG-1999) Viral Pathogenesis Division, Beth Israel Deaconess Medical Center, Research East 113, PO Box 15732, Boston, MA 02215, USA
395 CTGTATCTTCAAATGGACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAG 453
                                                                                                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                               1 (bases 1 to 463)
Helmuth, B.F., Letvin, N.L. and Margolin, D.H.
Germline repertoire of the immunoglobulin V(H)3 family in rhesus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="IGHV"
/note="similar to human immunoglobulin heavy chain
variable segments of the VH3 family; synonyms: IgVH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            457. .>463
/gene="IGHV"
/function="putative recombinant recognition sequence
(heptamer)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vortebrata; Eutele
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
9
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                                                                             AF173918
Macaca mulatta immunoglobulin heavy chain variable precursor (IGHV) gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 2.4e-58;
0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                        monkeys
Immunogenetics 51 (7), 519-527 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. 463
/organism="Macaca mulatta"
/mol_type="genomic DNA"
/db_xref="taxon:9544"
/tissue_type="kidney"
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/gene="IGHV"
                                                                                                                                                                                             Macaca mulatta (rhesus monkey)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                          AF173918.1 GI:9587768
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ilarity 93.0%;
Conservative
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Margolin, D.H.
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GFTFSDYYMDWVRQAPGKGLEWVSRISNGGGSTWYADSVKGRFTISRENAKNTLYLQM
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Submitted (02-AUG-1999) Viral Pathogenesis Division, Beth Israel
Deaconess Medical Center, Research East 113, PO Box 15732, Boston,
                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
1 (bases 1 to 463)
Helmuth, E.F., Letvin, N.L. and Margolin, D.H.
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                                                                                                                                         Helmuth, E.F., Letvin, N.L. and Margolin, D.H.
Germline repertoire of the immunoglobulin V(H)3 family in rhesus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  variable segments of the VH3 family; synonyms: IgVH, Ig
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/gene="IGHV"
/function="putative recombinant recognition sequence
(heptamer)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="similar to human immunoglobulin heavy
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                                                                                                                                                                                                                                                                                                                                                                                          'organism="Macaca mulatta"
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/db_xref="G1:9587771"
                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/db_xref="taxon:9544"
/tissue_type="kidney"
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                                 Macaca mulatta (rhesus monkey)
Macaca mulatta
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458 bp DNA linear PAT 27-AUG-2002 Human monoclonal antibody against TGF-beta-II receptor and medicainal use thereof.
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                                                                                                                                    GATCGAAGGGACAGTAACTGGGGGTTTGACTACTGGGGCCAGGGAGTCCTGGTCACCGTC 408
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229 TGGTACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGAAGGCCCAAGAACACACA 288
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                                                                 CTGTATCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGGAGA
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08-NOV-2000 JP 2000340216
SHINJI SAKAMOTO MASAFUMI KAWADA
C07K16/28,A61K39/395,A61P1/16,A61P9/04,A61P9/10,A61P9/10,
                                       241 CIGITICITCAAAIGAACAGCCIGAGAGCIGAGGACACGGCIGTCIAIIACIGIGCGAG-
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Human monoclonal antibody against TGF-beta-II receptor
medicinal use
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Pred. No. 1.3e-57, 
0; Mismatches 51
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JAPAN TOBACCO INC
OS Homo gapiens (human)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
_121 c 139 g 10
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JP 2001206899-A/2.
Homo sapiens (human)
Homo sapiens
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/protein id="AAL96421.1"
/db_xxref="c1:1974427.2"
/db_xxref="c1:19744272"
/translation="MRFGLSWYFLVALLKGVQGEVQIVESGGGLAKPGGSLRLSCAAS
GFTFSDYYMDWYRQAPGKGLEWYSRINYGGSTWYADSVKGRFTISRENAKNTLYLQMN
SIRABDTAVYYCARDRRDSNWGFDYWGQGVLVTVSSASASA"
                                                                                                                                                                                                                                                                        mRNA linear PRI 27-MAR-2002
VH3-d3 immunoglobulin heavy chain
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Scinicariello, F., Jayashankar, L. and Attanasio, R.
Baboon immunoglobulin variable region heavy chains: identification of genes homologous to members of the human IGHV1-IGHV7 subgroups Immunogenetics 53 (10-11), 815-820 (2002)
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Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Papio.
TCCTGCGCAGCCTCCG----GATTCACCTTCAGTGACTACTACATGGACTGGGTCCGC
                                                             TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAAGGCCAACAACACA
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Scinicariello, F., Jayashankar, L. and Attanasio, R.
Direct Submission
Submitted (104-SEP-2001) Department of Biology, Georgia State University, PO BOX 4010, Allanta, GA 30302, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
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                                                                                                                                                                                                                                                                          AF416355
Papio cynocephalus anubis clone VI
variable region mRNA, partial cds
AF416355
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/mol_type="mRNA"
/sub_species="anubis"
/db_xref="taxon:9555"
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                                                                                                                                                                                                                                                                                                                                                                                        Papio anubis (olive baboon)
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'codon_start=1
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ALIJOYZI 462 bp DNA linear PRI 31-JUL-2000
Macaca mulatta immunoglobulin heavy chain variable segment
precursor (IGHV) gene, partial cds.
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GFTFSDYYMHWVRQASGKGLEWVSRISNGGGSTWYADSVKGRFTISRENAKNTLYLQM
DSLRAEDTAVYYCARDTV"
                                       292 CTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGA 351
                   CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (Dasses 1 to 462)
Margolin, D.H.
Direct Submission.
Submitted (02-AUG-1999) Viral Pathogenesis Division, Beth Israel
Deaconess Medical Center, Research East 113, PO Box 15732, Boston,
                                                                                                                                                                                                                                                                                                                                                                                                      Cercopithecinae, Macaca.
1 (Dases 1 to 462)
Helmuth, E. F., Leevin, N. L. and Margolin, D. H.
Germline repertoire of the immunoglobulin V(H)3 family in rhesus
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/gene="IGHV"
/forbe="IGHV"
/note="similar to human immunoglobulin heavy chain
variable segments of the VH3 family; synonyms: IgVH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="immunoglobulin heavy chain variable segment
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                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae;
                                                                                         301 TIGACTACAGGGTCTGACTCCTGGGGCCCAGGGAGTCCTGGTCACCGTCTCCTCA
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Pred. No. 1.4e-56;
0; Mismatches 19;
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Immunogenetics 51 (7), 519-527 (2000)
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/organism="Macaca mulatta"
/mol_type="genomic DNA"
/db_xref="taxon:9544"
/tissue_type="kidney"
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/db_xref="GI:9587775"
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/codon_start=1
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/gene="IGHV"
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/gene="IGHV"
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nilarity 91.6%;
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TACTACACACACACTCAGTGAAGGCCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCA 291
                                                       CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
                                                                              Human monoclonal antibody for human TGF-beta type II receptor
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                                                                                                                                                                                                                                      458 bp DNA linear PAT 27-AUG-200 Human monoclonal antibody for human TGF-beta type II receptor and pharmaceutical use thereof.
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PR 18-NOV-1999 JP 99P 328681,08-NOV-2000 JP 00P 340216 PI
SHINJI SAKAMOTO, MASATWI KAMADA
PC C12N15/13,C07K16/28,C12N5/16,A61K39/395,A61P43/00,A61P13/12,
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JAPAN TOBACCO INC. SHINJI SAKAMOTO, MASAFUMI KAMADA OS Homo sapiens (human)
PW WO 013642-A/2
PD 25-MAY-2001
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Pred. No. 1.3e-57;
0; Mismatches 51
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Best Local Similarity 83.9%;
Matches 297; Conservative
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/codon start=1
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/producft="anti-1FN-G scFv"
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/db_xref="di:3152374"
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LEWQALSGSGGSTYADSYKGRFTISRDNSKNTLYLQMNSIRAEDTAVYYCAKRAPA
FDYWQGTLVTVSSCGGSGGGGASTGEIULTQSPGERATLSCRASQSVS
SSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGGTDFTLTISRLEPEDFAVYY</pre>
                                                                                                                                                                                                                                                                                                   HSA6119 714 bp mRNA linear PRI 18-NOV-1998
Homo sapiens mRNA for A4 anti-IFN-G scFv recombinant antibody,
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Neri,D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Design and use of a phage display library. Human antibodies with subnanomolar affinity against a marker of angiogenesis eluted from a two-dimensional gel J. Biol. Chem. 273 (34), 21769-21776 (1998) 98371014
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                                             CAGGCTCCAGGCCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
                                                                                                    CAGGCTTCAGGGAAAGGGGCTGGAGTCTCACGTATTAGTAATGGTGGTGGTGGTAGCACA 333
                                                                                                                                            Direct Submission
Submitted (12-MAY-1998) Viti F., Molecular Biology and Biophysics,
ETH (Swiss Federal Institute of Technology), ETH Hoenggerberg,
CH-8093 Zuerich, SWITZERLAND
Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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GAGGTGCAGCTGGTGGAGTCTGGGGGGGCGTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
                            TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC
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/db_xref="taxon:9606"
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ilarity 83.4%;
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Homo sapiens
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Best Local Similarity
Matches 292; Conserv
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AUTHORS
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MEDLINE
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JOURNAL
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KEYWORDS
SOURCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 364)
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TCCTGTGCAGCCTCTG-----GATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGC
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                                                                             CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA
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Location/Qualiflers
1. .364
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PF 07-DEC-2000 JP 2000373259
PT KIYOTOSHI KANEKO
FC G01N33/53,C12N15/09,C12P21/08,C12Q1/68,C12N15/00
For screening high-efficiency antibody FH Key
Location/Qualifiers
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Method for screening high-efficiency antibody.
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82.0%; Pred. No. 7.1e-56;
tive 0; Mismatches 57;
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/90 c 114 g 7
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JP 2002174635-A/164
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JP 2002174635-A/164.
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Homo sapiens
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Matches 287; Conservative
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Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/clone_lib="AIMS4"
/note="mixture of tissues:tonsils, umbilical cords,
peripheral blood and bone marrow"
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Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyake 470-1192, Japan
(B-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.
NNNNNNNNNNNNNNTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC 352
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Pred. No. 1.2e-55;
0; Mismatches 53
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Best Local Similarity 83.1%;
Matches 291; Conservative
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Patent: WO 0242774-A 164 30-MAY-2002;
ADANN SCIENCE AND TECHNOLOGY CORP, JAPAN AS REPRESENTED BY
PRESIDENT O KAZUHIKO KATAYAMA PSACHIATRY MINISTRY OF HEALTH LABOUR
AND WELFARE, KIYOTOSHI KANEKO
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 364)
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Location/Qualifiers
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Pred. No. 7.1e-56;
0; Mismatches 57; Indels
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
a 90 c 114 g 75
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05-JUN-2001 WO 2001JP004732
24-NOV-2000 JP 00P 358539
KIXOTOSHI KANEKO
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High efficiency scree
Location/Qualifiers
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WO 0242774-A/164
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Best Local Similarity 82.0%;
Matches 287; Conservative
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Homo sapiens (human)
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PRI 15-FEB-1999

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                                                                                 241 CTGTTTCTTCAAATGAACAGCCTGAGGACACGGACACGGCTGTCTATTACTGTGCGAGC 300
                                                                                                       Department of Medicine - 0663,
La Jolla, California
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 429) Olee, T., Lu, E.W., Huang, D.F., Soto-Gil, R.W., Deftos, M., Kozin, F., Garson, D.A., and Chen, P.P. Generic analysis of self-associating immunoglobulin G rheumatoid factors from two rheumatoid synovia implicates an antigen-driven
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Homo sapiens rearranged Humigha3dl gene encoding IgG heavy chain
Variable region.
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                               181 TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAAACGCCAACACAACA
                                                                                                                                                                                                                                                                                                                                            X59703.1 GI:32012
heavy chain; IgG; immunoglobulin; J-segment; variable region.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                          295 GIGGGAGCTICCCAIGACTACTGGGGCCAGGGAACCCTGGICACGICTCCICA 348
                                                                                                                                                         301 TTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 354
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Pred. No. 2.2e-55;
0; Mismatches 48
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92156804
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University of California, San Diego
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
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1..429
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/gene="Humigha3d1"
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Best Local Similarity 84.0%;
Matches 300; Conservative 0
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2 (bases 1 to 429)
Tsaiwei,0.
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Human immunoglobulin heavy chain variable region (clone Amulc3-3)
U00491
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LEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAMVGAS
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(Dases 1 to 348)

Huang, C. and Stollar, B.D.

A majority of 19 H chain cDNA of normal human adult blood

lymphocytes resembles cDNA for fetal Ig and natural autoantibodies
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                                                       CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
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TACTACGCAGACTCTGTGAAGGCCGATTCACCATCTCCAGAGACAACGCCAAAGAACTCA
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                                                                                                                           301 TTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC 350
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Stollar, B.D.
Direct Submission
Submitted (10-AUG-1993) Stollar B.D., Tufts University,
Biochemistry, 136 Harrison Ave., Boston, MA 02111, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 242.4; DB 9; Length 348; Pred. No. 2e-55; 0; Mismatches 56; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="B-lymphocyte"
/tissue type="peripheral blood"
/clone_lib="Amu2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="Amulc3-3"
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91 c 11
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Best Local Similarity 82.5%;
Matches 292; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sex="male"
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
Homo sapiens
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GFTFSNYSMNWVRQAPGKGLEWVSYISSSSTIYYADSVKGRFTISRDNAKNSLYLOM
NSLRAEDTAVYYCARSGYRGGDYWGQGTLVTVSSASTKGPSVPPLAPCSRSTSGGTAA
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oin(79. .124.228. .>667)
gene="humha3d1"
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'protein id="AAA20444.1"
db_xref="G1:520410"
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                                                                                  CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
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(bases 20 to 532)

Deffos, M., Olee, T., Carson, D.A. and Chen, P.P.

Defining the genetic origins of three rheumatoid synovium-derived IgG rheumatoid factors
                                                                                                                                                                                                                                                                                                                                                                                                     HSU03894 667 bp DNA linear PRI 22-OCT-20
Human rheumatoid factor D1 IgG heavy chain VH3 region rearranged
(humha3d1) gene, partial cds.
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Direct Submission
Submitted (01-DEC-1993) Pojen P. Chen, Medicine, 'California San Diego, 9500 Gilman Dr., La Jolla,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Clin. Invest. 93 (6), 2545-2553 (1994)
94259815
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| Organism="Homo sapiens" |
| Mool_type="genomic DNA" |
| db xref="teaxon:9606" |
| cell_line="D1 hybridoma" |
| cisue_type="lymphocyte" |
| cisue_type="synovium" |
| dev_stage="adult" |
| note="rearranged" |
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/gene="humha3d1"
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/gene="humha3d1"
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/gene="humha3d1"
/product="rheumatoid factor D1 IgG heavy chain VH3 region"
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Pred. No. 2.1e-55;
0; Mismatches 48;
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ne : 1468.44 secs
                                                                                                                                      Query Match 68.4%;
Best Local Similarity 84.0%;
Matches 300; Conservative
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Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Database :

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AW#U1971
UI-HP-BKO-aao-c-04-0-UI.r1 NIH MGC_36 Homo sapiens cDNA clone
IMAGE:3054342 5', mRNA sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 406)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbe-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                              BQ711355
BX357384
BQ710859
BG757947
BG754024
BQ706723
BQ706746
BM914329
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BM713479
BQ712666
BQ708408
BQ709879
AW403862
BG757960
AW408316
                                                                               BQ708458
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BG684839
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BG686881
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AW403707
                                       AW401428
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Homo sapiens
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BX379829 BX379829
BX417408 BX417408
BM007475 603616742
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                                                                     December 29, 2003, 16:08:50 ; Search time 1531.8 Seconds (without alignments) 5616.780 Million cell updates/sec
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        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                             22781392 segs, 12152238056 residues
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Score

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241.4 239.2 239.2 235.8

BQ707926 AGENCOURT BQ712092 AGENCOURT BG771903 602721715 BG745545 602723942

BQ894558 AGENCOURT

CA397705 CS94 F63.7 BG68 68 B1 G026 508 67 A440834 U.1F-BK0 BG39796 G024 3948 BG75974 BG75974 BG75974 BG75974 BG77974 G0271146 BG779794 G0271146 BG779794 G02714983 BG77947 G02714983 BG75947 G02714983 BG75947 GGNCOURT BG9706746 AGENCOURT BG9706746 AGENCOURT BG756 GGNCOURT BG766 AGENCOURT BG766 AGENCOURT BG766 AGENCOURT BG766 AGENCOURT BG711025 AGENCOURT BG711025 AGENCOURT BG711025 AGENCOURT BG71104 AGENCOURT BG71105 AGENCOURT AGENCOURT AGENC

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AW401428 UI-HF-BK0 AW401386 UI-HF-BK0 BG340670 602462250

AJ547930 AJ547930

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: fliang@lifetech.com
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/ tissue_type="lymph"
/ cell_type="germinal center B cells"
/ cell_line="MGGBS"
/ lab_fnot="width GLTJ"
/ clone lib="NHH MGC 36"
/ note="Vector: pTyT3-Pac; Site_1: NotI; Site_2: Eco RI;
/ clone lib="NHH MGC 36"
/ note="Vector: pTyT3-Pac; Site_1: NotI; Site_2: Eco RI;
/ clone lib="Nut MGC 36"
/ note="Vector: pTyT3-Pac; Site_1: NotI; Site_2: Eco RI;
/ clone lib="Nut MHH MGC 36"
/ constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. and M. Bento Soares, Ph.D."

Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 1138)

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cgi-bin/cluster.cgi?seq=CSODI040BC08QP1&cluster=7198.r. Contact
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r
more information about this cluster, see
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                       68.2%; Score 241.4; DB 9
82.2%; Pred. No. 3.2e-52;
iive 0; Mismatches 57
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   Location/Qualifiers
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BX417408 Homo sapiens PLACENTA Homo sapiens CDNA clone CSODE009Y115
5-PRIME, mRNA sequence.
BX417408
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                       /mol_type="mRNA"
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/clone=Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
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/note="lst strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.

323 c 329 g 225 t 11 others
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cgi-bin/cluster.cgi?seq=CSODE009AE08QPl&cluster=7198.r. Contact
Feng Liang Email : fliang@lifetech.com URL :
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Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI040BC08QP1.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r
more information about this cluster, see
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.6%; Score 239.2; DB 13; Length 1138;
llarity 81.9%; Pred. No. 1.7e-51;
Conservative 0; Mismatches 58; Indels 6;
                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                   Location/Qualifiers
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High quality sequence stop: 608
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                                                                                                 /mol_type="mRNA"
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//db xxef="texon:9606"
//clone="csObBoO9Y115"
//tissue type="PLACENTA"
//clone lib="Homo saphens PLACENTA"
//note="Vector: PCMVSPORT 6; 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, with a Not1-oligo(dT) primer. Five prime end enriched, the Not I and CoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 613)
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National Institutes of Health, Mammalian Gene Collection (MGC)
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODE009AE08QP1. Location/Qualifiers
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Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can k
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM1913 row: d column: 12
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/mol_type="mRNA"
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/db xref="IMAGE:5440475"
/lab host="IMAGE:5440475"
/lab host="DHIOB (phage-resistant)"
/clone lib="NHH MGC 113"
/clone lib="NHH MGC 113"
/note="Organ: spleen; Vector: pOTB7; Site_1: Xho1; Site_2:
FCORI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/Xho1 sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ....v./>35
UI-HF-BKO-aaq-a-05-0-UI.rl NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3054608 5', mRNA sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (basea 1 to 447n)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can be
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Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDN Library Preparation: M.B. Soares Lab
CDN Library Arrayed by: M.B. Soares Lab
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Pred. No. 1.1e-50;
0; Mismatches 52
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                             l. .613
/organism="Homo sapiens"
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Location/Qualifiers
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Best Local Similarity 82.9%;
Matches 296; Conservative
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AW403220.1 GI:6922096
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Best Local Similarity 81.8%;
Matches 297; Conservative
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                  Length 447;
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Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
                                                                                                                                                                                                                                                                                                                                                               62; Indels
found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seg primer: M13 Forward.
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Pred. No. 5.6e-50;
0; Mismatches 62
                                                                             organism="Homo sapiens"
                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3054608"
                                             Location/Qualifiers
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Homo sapiens
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Best Local S
Matches 286
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SOURCE
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JOURNAL
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AW402613
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/u. 3.1. /
/ Crganism="Homo sapiens"
/ Mol Type="mRNA"
/ Mol Type="mRNA"
/ Ab Type="Lymph"
/ Lissue_type="lymph"
/ Cell_type="germinal center B cells"
/ Cell_line="MGC85"
/ Lab Fost="DH10B (LTI)"
/ Clone lib="MNH MGC.36"
/ Note="Vector: pT7T9-Pac; Site_1: Not!; Site_2: Eco RI;
/ Note="Vector: pT7T9-Pac; Site_1: Not!; Site_1: N
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UI-HF-BKO-aay-h-04-0-UI.rl NIH MGC_36 Homo sapiens cDNA clone
IMAGE:3055710 5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbp/image/image.html
Seq primer: M13 Forward.
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Pred. No. 1.4e-49;
0; Mismatches 51,
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Similarity
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Best Local Simil
Matches 298; (
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                                                        REFERENCE
AUTHORS
TITLE
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| /note: pT77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 GAGGTGCAGCTGGTGGAGTCTGGGGGGAGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCTGTGCAGCCTCTG-----GATTCACTTCAGTAGCGATAGCATGAACTGGGTCCGC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTAGTAGTAGTTGTTTCATA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 TACTACGCAGACTCAGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCA 309
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                  Email: cgapbs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Stadd, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can I

Clond through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.0%; Score 230.2; DB 9; Length 471; 81.3%; Pred. No. 2.7e-49; Indels 21; ive 0; Mismatches 48; Indels 21;
Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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Homo sapiens
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Best Local S:
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Site_2: BcoRI; cDNA made by oligo-dT priming.
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Site_2: BcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/Xhol sites using the following 5' adaptor: GGCAGAG(G). Size-selected by Ling for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscribt II RT (Life Technologies).
Note: this is a NIH-MGC Library."
                                                                                                                                                           In Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM1209 row: g column: 06
High quality sequence stop: 696.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
   Craniata; Vertebrata; Euteleostomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 AGGTGCAGCTGGTGGAGTCTGGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 CCTGTGCAGCCTCTG----GATTCACCTTCAGTGACTACATGAGCTGGATCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u> AGGTGCAGCTGGTGGAGTCTGGGGGGGGCGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTCT</u>
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                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                   Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Pred. No. 1.8e-48;
0; Mismatches 49
Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
1 (bases 1 to 1164)
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ilarity 81.0%;
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AW401386.1 GI:6920168
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AW401428 16-FEB-2000 UL-HF-BKO-aad-b-02-0-UI.rl NIH MGC_36 Homo sapiens CDNA clone IMAGE:3053139 5', mRNA sequence.
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                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I bases I to 443)
NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image.html
Seq primer: M13 Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                               AW401428.1 GI:6920011
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                                                                                                                                                                     Homo sapiens (human)
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Matches 295
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AM401386 S82 bp mRNA linear EST 16-FEB-2000
UI-FR-BKO-aau-h-03-0-UI.rl NIH MGC_36 Homo sapiens cDNA clone
IMAGE:3055324 5', mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Sass) to 582)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Except Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Bco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: Ml3 Forward.
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80.8%; Pred. No. 7.4e-48;
iive 0; Mismatches 57;
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AJ547930 ATAPHEU Medicago truncatula cDNA clone mtaehac110006d09, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Colditz, F., Rosendahl, S., Bekel, T., Meyer, F., Kuester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ctaatacgactcactatagggcagcgtggtcgcggccgaggt (Clontech) and
ligated after Suppression Subtractive Hybridization into
the pGEM-Teasy vector (Promega). Plasmids containing cDNA
inserts were propagated in E. coli TOP 10F' cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 gagerecageregagareregagagagagagarecageeragagagareeragagaere 149
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                       121 CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 300
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Nyamauren,O., Colditz,F., Rosendahl,S., Bekel,T., Meyer,F., Kueste, H., Franken,P. and Krajinski,F.
First insights into the pathogenic interaction formed between the comycete Aphanomyces euteiches and legumes using the model plant Medicago truncatula
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/organism=""
/organism=""
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/clone="mtaehac11006d09"
/tissue_type="foot"
/tev stage="6 days afer inoculation with Aphanomyces eutelches zoospores"
                                                                                     Length 429;
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LG Molekulargenetik
Herrenhaeuser Str. 2 D-10419 Hannover, Germany.
Location/Qualifiers
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80.1%; Pred. No. 1.7e-47;
ive 0; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Medicago truncatula"
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                                                                                                                                                                                                                                                                                                                                                                                        Medicago truncatula (barrel medic)
Medicago truncatula
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109 c
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es 277; Conserv
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    ਨੇ
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/tissue_type="primary B-cells from tonsils (cell line)"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the pirectionally cloned into EcoRI/XhoI sites aclected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                            BG340670 648 bp mRNA linear EST 27-FEB-2001 602462250F1 NIH_MGC_48 Homo gapiens cDNA clone IMAGE:4574941 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                              426 GCTATTTTGACTGGTAGCCTTGACTGCTGGGGGCCCAGGGGACCCTGGTCACCGTCTCCTCA 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
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    298 ---AGCTTGACTACAGGGTCTGACTCCTGGGCCCAGGGAGTCCTGGTCACCGTCTCCTCA 354
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                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 648)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM1285 row: d column: 14
High quality sequence stop: 648.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAGGTGCAGCTGGTGGAGTCTGGGGGGGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
                                                                                                                                                                                                                                                                                                                                                                                                           NIN-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tsaue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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Pred. No. 9.7e-48;
0; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                      BG340670.1 GI:13147108
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Best Local Similarity 81.4%;
Matches 288; Conservative
                                                                                                                                                                                                                                                                                                   sapiens (human)
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                                                                                                                                                                                                         mRNA sequence.
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Homo sapiens
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                                                                                                                                                                                 DEFINITION
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TITLE
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BG340670
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Gaps

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/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ711467 920 bp mRNA linear EST 16-JUL-2002 AGENCOURT 8484867 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6300988 BQ711467
                                                                                                                                                                                                          241 CIGITICITCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGA-- 298
                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tisaue Procurement: Dr. Mark Watson
Tisaue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioseience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2516 row: c column: 05
High quality sequence stop: 587.
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                       CAGGCTCCAGGGCCAGGGCTGGGAGTCGCTCTCACGTATTAGTAGTGGTGGTGATCCCACA 180
                                                                                                                                                                                                                                                                                                    299 ----GCTTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (Dases 1 to 920)
NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                               TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol type="mRNA"
/db xref="taxon.9606"
/clone="IMAGE:6300989"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
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Homo sapiens
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Best Local Similarity 80.1;
Matches 293; Conservative
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/organism="Homo sapiens"
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/db xref="taxon:9606"
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/clone="INHAGE:6214426"
/clone="Drygan: spleen; Vector: poTB7; Site 1: XhoI; Site_2:
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/note="Organ: spleen; Vector: poTB7; Site_1: Anote: contains and spleen; vector: spleen; Vector: contains and Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                    920 bp mRNA linear EST 16-JUL-2002
.7976428 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:6214426
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                                                                         TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACA 240
                                                                                                 TACTACGCAGACTCCGTGAAGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACAC 323
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NIH-MGC http://mgc.nci.nih.gov/.
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1 GAGGTGCAGCTGGTGGAGTCTGGGGGGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM3381 row: I column: 11
High quality sequence stop: 649.
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                                                                                                                                                                                                                                                                                        384 GGGAATTCGCGGCGGAGGCAGTGGGGCCAAGGTACCCTGGTCCACCG 429
                                                                                                                                                                                                                                                              301 TTGACTACAGGGTCTGACTCCTGGGGCCCAGGGAGTCCTGGTCACCG 346
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Pred. No. 2.3e-47;
0; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
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80.6%;
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Homo sapiens
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5', mRNA Bequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW403059 456 bp mRNA linear EST 16-FEB-2000 UI-HF-BK0-aai-f-10-0-UI.rl NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054090 5', mRNA sequence.
                                                                                                                                                284 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACAG 343
180
                                                                                                                      TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_aref="taxon:9606"
/db_aref="taxon:9606"
/db_aref="taxon:9606"
/clone="taxon:9606"
/clone="Vector: pr773-Pac; Site_1: Not; Site_2: Eco RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Scares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 4.5e-47;
0; Mismatches 49; Indels 6;
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Best Local Similarity 82.9
Matches 267; Conservative
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Anti-murine CTLA-4 TRO005 heavy chain DNA encoding anti-Anti-TRAIL-R antib

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Anti-human CD23 5E8 moclonal antibody heavy chain variable region DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 does not contain a stop codon"
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/note= "encodes CDR 1 region"
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                                                                                                      December 29, 2003, 16:08:50 ; Search time 154.453 Seconds (without alignments) 6187.013 Million cell updates/sec
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
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1 GAGGIGCAGCIGGAGIC......ICCIGGICACCGICICCCICA
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                GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                            nucleic search, using sw model
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AAV61794
AAH41153
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/note= "encodes CDR 2 region"
358..378
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98US-0019441.
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homologous recombination; vector; neomycin phosphotransferase;
neo gene; selectable marker; immunoglobulin; CD23; 5E8; human;
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                                                                                                                                 Traget plasmid Mandy containing anti-CD23 gene.

    Cytomegalovirus.
    Rhesus macaque polyoma virus.

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    Photinus sp.
    Salmonella typhimurium.
    Homo sapiens.

AAV61794 standard; DNA; 19035 BP.
                                                                                                                                                                                                                                                                               Mus sp.
Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                misc_feature
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barnett
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This is the nucleotide sequence of novel target plasmid Mandy.

The plasmid includes an inactivated murine dihydrofolate reductase (DHRR) gene, the Escherichia coll beta-galactosidase gene, baculovirus DNA, a casette comprising the promoter and enhancer elements from cytomegalovirus and SV40 virus, the E. coli heta-glucuronidase (GUS) gene, firefly luciferses gene, an inactivated Salmonella typhimurium histidinol dehydrogenase (HisD) gene and transposon This neowycin phosphotransferase (neo) gene sequences, in a pBR-derived backbone, and also an anti-human CD23 igs receptor human gamma-1 monoclonal antibody 5E8 gene. The invention provides a novel method for integrating a desired invention provides a novel method for integrating desired invention provides a target site within the genome of a mammalian cell with a 'marker plasmid' such as Deemond (see AAV61782), which contains a unique sequence that is foreign to the mammalian cell with a warker plasmid, such as Deemond (see AAV61782), which contains a unique sequence that is foreign to the mammalian cell ollowed by transfection with a 'target plasmid', such as Mandy or Molly (see AAV61793), containing a sequence which provides for homologous recombination with the unique sequence which provides for homologous recombination system utilises the neo gene as a communant selectable marker. The neo gene is split into 3 exons. Exon 3 is present on the marker plasmid and becomes integrated into the mammalian cells, the marker plasmid into the mammalian cells split into 3 exons. Exon 3 is present on the marker plasmid and 2 are present on the marker plasmid and 2 least one of interest is cloned. Homologous recombination with the unique sequence which the contraction of the marker is cloned. Homologous recombination and are separated by an intron into which at the barder of interest is cloned. Homologous recombination and are separated by an interning a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mammalian cells, and can be used to express any type of recombinant protein. The use of a triply spliced selectable marker means that all selected colonies arise from homologous recombination. In addition, the number of colonies that need to be screened to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the targeting vector with the integrated marking vector results in correct splicing of all 3 exons of the neo gene and expression of a functional neo protein. The method is applicable to all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 19; Length 19035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             An amplifiable gene vector, so that when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is targeted to this site, the gene is further enhanced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19035 BP; 4705 A; 4968 C; 4822 G; 4519 T; 21 other;
- comprises homologous recombination using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             identify high producer clones is reduced. An amp
be inserted on integration of the marking vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 349.2; DB
Pred. No. 2e-88;
0; Mismatches
                        selectable marker and target plasmids
                                                                                     Example 1; Fig 10; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.6%;
99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
   immunoglobulins
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9608 9548 ö 120 180 09 9549 TCCTGCGCAGCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 9489 GAGGTGCAGCTGGTGGAGTCTGGGGGGGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC CAGGCTCCAGGGCAGGGGCTGGAGTCGCTCTCACGTATTAGTAGTAGTGGTGATCCCACA <u> GAGGTGCAGCTGGTGGAGTCTGGGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC</u> TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 0; Gaps Indels 3, 351; Conservative ч 121 61 Best Loc Matches 셤 8 à g ò

9728 9668 240 TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACA 181 셤 S . 6

CTGTTTCTTCAAATGAACAGCCTGAGGACTGACGACACGGCTGTCTATTACTGTGCGAGC 9729 CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC

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301 TTGACTACAGGGTCTGACTCCTGGGCCAGGGAGTCCTGGTCACGTCTCCTCA 354

9788

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121 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
CIGITICITCAAAIGAACAGCCIGAGAGCIGAGACACGGCIGICIATIACIGIGCGAGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 1, 78pp, Japanese
                                                                                                                                                                            BP
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larity 82.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-NOV-2000; 2000JP-0358539.
                                                                                                                                                                            standard; DNA; 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-2001; 2001WO-JP04732
                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-471742/50.
P-PSDB; AAO21548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 287; Conserv
                                                                                                                                                                                                                                                                                                                                                                                     WO200242774-A1
                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                         02-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2002
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                                                                                                                                                                            AAL39119
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                                                                                                                                                                                                           AAL39119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to novel human monoclonal antibodies. The antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II receptor, resulting in the inhibition of the signal transduction of human TGF-beta into cells. The antibodies can be used for the prevention and treatment of diseases associated with the production of TGF-beta, such as tissue fibrosis in the lung, liver, skin, kidney or other tissues, atherosclerosis, atopy, keloid and arthritis. The present sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGIGCAGCIGGAGGICTGGGGGGGGGCCIGGTCAAGCCIGGGGGGGTCCCTGAGACTC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAAGGCCAACAACACACA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        recreteceaccierce----carreactricacracerrageardaacracec 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                         Human, antiarthritic; cardiant; monoclonal antibody; keloid; arthritis; Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy; signal transduction inhibition; tissue fibrosis; atherosclerosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGGTGCAGCTGGTGGAGTCTGGGGGGCGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGGCTCCAGGGAAGGGGCTGGAGTCGATCCATTAGTAGTAGTAGTAGTACATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
9789 TIGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCCACCGTCTCCTCA 9842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human monoclonal antibodies recognizing human TGF-beta II receptor, useful for treating TGF-beta associated diseases such as tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 458 BP; 92 A; 121 C; 139 G; 106 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.7%; Score 250.4; DB 2 ilarity 83.9%; Pred. No. 5.6e-61; Conservative 0; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 12; Page 94-95; 118pp; Japanese.
                                                                                                                                                                                             sequence SEQ ID 3.
                                                                                                 ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                     17-NOV-2000; 2000WO-JP08129
                                                                                                                                                                                                                                                                                                                                                                                                                    99JP-0328681
                                                                                                                                                                                                                                                                                                                                                                                                                                   08-NOV-2000; 2000JP-0340216
                                                                                                 AAH41153 standard; DNA; 458
                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kamada M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-343825/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                          WO200136642-A1
                                                                                                                                                                                             coding
                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                  18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sakamoto S,
                                                                                                                                                               22-AUG-2001
                                                                                                                                                                                                                                                                                                                                                       25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                AAH41153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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AAH41153
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292 CTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel method for screening an antibody, comprising performing 2-D electrophoresis on plural proteins in a sample. Individual protein spots are separated by reacting them with an antibody library and then replicating the bound antibodies before reacting them with the spot proteins again. The method is useful for screening an antibody specific for a target protein, e.g. from a phage antibody library, which is useful in proteomics for studying various protein and complementary deoxyribonucleic acid (cDMA) expression libraries as well as gene functions, and in other biological and medical sciences. This polynucleotide is a DNA sequence relating to the antibody screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening antibody, 2-D electrophoresis, plural protein, protein spot, antibody library, proteomics, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Screening an antibody using 2-D electrophoresis on plural proteins in samples for separating individual protein spots to react with an antibody library useful in proteomics and other biological sciences -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAGGTGCAGCTGTTGGAGTCTCGGGGAGGCTTGGTACAGCCTGGGGGCTCCCTGAGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rccrerecascerers ---- sarreacerrrascascrarecerrascrasseres
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                                                                                                                                                             GGTACTGGGGGTTTGACTACTGGGGCCAGGAACCCTGGTCACGTCTCCTCA 405
                                                                                                                     301 TIGACTACAGGGICTGACTCCTGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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Pred. No. 3.3e-59;
0; Mismatches 57; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 348 BP; 71 A; 84 C; 108 G; 73 T; 12 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibody screening method related DNA VH(DP-47)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JAPAN SCI & TECHNOLOGY CORP.
JAPAN NAT CENT NEUROLOGY & PSYCHIATRY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to screening an antibody against a specific protein in an objective structure sample containing a protein group in high efficiency, comprising reacting an objective structure sample containing a protein group or a portion containing an objective protein in the sample with an antibody library, recovering the antibody combined with the protein, replicating the recovered antibody and reacting it with the objective protein at least once. The method is used for the identification of an objective protein. The present sequence is a DNA sequence for an antibody chain (derived from the DP47 heavy chain, the DPK22 light chain or a combination of the two) used in the method of
CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACA 174
                                              TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACA 240
                                                                   175 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACG 234
                                                                                                             CTGTTTCTTCAAATGAACAGCCTGAGAGCTGACACGGCTGTCTATTACTGTGCGAGC 300
                                                                                                                                     CTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Screening of an antibody used for the identification of an objective protein in high efficiency -
                                                                                                                                                                           301 TTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC 350
                                                                                                                                                                                          295 NANNANANANTTTGACTACTGGGGCCAGGGAACCTGGTCACCGTCTC 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 244; DB 24; Length 364;
Pred. No. 3.4e-59;
0; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                     for antibody DP47 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence arrayed library; SAL; ss; antibody library; protein identification; DP47; DPK22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 364 BP; 73 A; 90 C; 114 G; 75 T; 12 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KAGAKU GIJUTSU SHINKO JIGYODAN.
KOKURITSU SEISHIN SHINKEI CENT SOCHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 8; Page 38; 43pp; Japanese.
                                                                                                                                                                                                                                                                                         ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tch 68.9%;
sal Similarity 82.0%;
287; Conservative (
                                                                                                                                                                                                                                                                                         ABK99213 standard; DNA; 364
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                                                                                                                                                                                                                                                                                                                                                      (first entry)
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P-PSDB; ABG69320.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the invention
                                                                                                                                                                                                                                                                                                                                                                                     DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                       21-OCT-2002
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Best Local S
Matches 287
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TCCTGTGCAGCCTCTG----GATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGC 122
                                                     180
                                                                                         182
                                                                                                                                                                                                                       CIGIAICTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel method for screening an antibody, comprising performing 2-D electrophoresis on plural proteins in a sample. Individual proteins are separated by reacting them with an antibody library and then replicating the bound antibodies before reacting them with the spot proteins again. The method is useful for screening an antibody specific for a target protein, e.g. from a phage antibody library, which is useful in proteomics for studying various protein and complementary decayribonucle acid (CDNA) expression libraries as well as gene functions, and in other biological and medical sciences. This polynucleotide is a DNA sequence relating to the antibody screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening antibody; 2-D electrophoresis; plural protein; protein spot; antibody library; proteomics; ds.
                                                                             Screening an antibody using 2-D electrophoresis on plural proteins in samples for separating individual protein spots to react with an antibody library useful in proteomics and other biological sciences -
                                                       CAGGCTCCAGGGCAGGGCTGGAGTGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA
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Pred. No. 3.4e-59;
0; Mismatches 57; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibody screening method related DNA SEQ ID No 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 364 BP; 73 A; 90 C; 114 G; 75 T; 12 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NISC-) JAPAN SCI & TECHNOLOGY CORP.
(NINA-) JAPAN NAT CENT NEUROLOGY & PSYCHIATRY.
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Best Local Similarity 82.0%;
Matches 287; Conservative
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                                                                                                                                                                                         TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACG 242
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                                                                 CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
                                                                                                                                                                         TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGGAACGCCAACAACACA 240
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                              GAGGTGCAGCTGGTGGAGTCTGGGGGGGGGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTC
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                                                                                                                                                                                                                                                                                  301 TIGACTACAGGGICIGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening; functional polypeptide; ligand; non-functional; enrichment; single chain antibody; ScFv; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening for functional polypeptides which bind a ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding a single chain antibody (ScFv)
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P-PSDB; AAY02472.
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diagnostic, prophylactic and therapeutic procedures. The present sequence encodes the single chain antibody (ScFv) that forms the basis of a library according to the invention.
                                                                                                                                                                 1 GAGGTGCAGCTGGAGTCTGGGGGCGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
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                                                                                                                                                                                                                               TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC
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                                                                                                                                  Gaps
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/note= "no start or stop codons given"
                                                                                               Score 240; DB 20; Length 720;
Pred. No. 5.5e-58;
0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 720 BP; 168 A; 181 C; 214 G; 157 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human serum albumin antibody related DNA #1
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                                                                                                    67.8%;
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Synthetic.
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Homo sapiens.

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The present invention describes a dual-specific ligand (I) comprising:

(a) a first single immunoglobulin variable domain with a binding specificity to a first antieve.

(a) second complementary immunoglobulin single variable domain with a binding activity to a second antigen or epitope. The binding domains are mutually complementary, and the first and second domains lack mutually complementary domains that share the same specificity. (I) has cytostatic, anti-HIV, antianaemic, antiinflammatory, immunosuppressive and neuroprotective activities. The dual-specific ligand is useful for treating, preventing or diagnosing inflammations or autoimmune disorders (e.g. multiple sclerosis, Crohn's disease or myasthenia gravis). The dual-specific ligand may be used to recruit cytotoxic T-cells to a cancer cell. The dual-specific ligand is also useful for monitoring the efficacy of drugs, as well as for monitoring toxicity. The present sequence encodes a human serum albumin (HSA) related antibody sequence, which is used in an example from the
                                                                         Dual-specific ligand having immunoglobulins with binding specificity different antigens or epitopes, useful for treating, preventing or diagnosing diseases, e.g. cancer, HIV infection, inflammations, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 720 BP; 168 A; 181 C; 214 G; 157 T; 0 other;
                                                                                                                                                                                                            Example 1; Fig 1; 84pp; English.
WPI; 2003-210246/20.
P-PSDB; ABP95997.
                                                                                                                                                           myasthenia gravis
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TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACATGGACTGGGTCCGC 120
                                                                                                                                                                                                                                                                                                                                    CTGTATICTGCAAATGAACAGCCTGAGAGCGGAGACACGGCCGTATATTACTGTGCGAAA 294
                                                                                                                                                                                                           TCCTGTGCAGCCTCTG-----GATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGC 114
                                                                                                                                                                                                                                                   CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
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67.8%; Score 240; DB 25; Length 720; llarity 82.6%; Pred. No. 5.5e-58; Conservative 0; Mismatches 55; Indels 6
                     Similarity
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Human; tumour; vascular endothelial growth factor receptor; metastasis; epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC; breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; gene; VH; ds.
                                                                                                       Human KDR (VEGFR-2) Fab heavy chain (VH) DNA from D2C6 clone.
AAD46290 standard; DNA; 348 BP
                                                                    (first entry)
                                                                  27-DEC-2002
                                  AAD46290;
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The interaction features to a method of initizating tumour growth factor receptor (VEGFR) antagonists in combination with radiation, chemotherapeutic agent, or epidermal growth factor receptor (EGFR) antagonists. The method is useful for inhibiting tumour growth in a human, where the tumour (e.g. tumour of the breast, heart, lung, small intestine, colon, spleen, bone, kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin, bone marrow, blood, thymus, uterus, testicles, cervix or liver) over expresses VEGFR. It is also useful for inhibiting growth of colon tumour or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR. It is preferably useful for treating subjects with both solid tumours, preferably useful tumours and non-solid tumours, preferably high vascular tumours and non-solid tumours. The inhibition of the progression of tumour includes prevention or inhibition of the progression of tumour includes the invasiveness, metastasis, recurrence and increase in size of the tumour. The present sequence is tumour KDR (VEGFR-2) Fab antibody heavy chain DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting tumor growth in humans involves administering vascular endothelial growth factor receptor antagonists in combination with radiation, chemotherapeutic agents, or epidermal growth factor receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method of inhibiting tumour growth which
                                                                                                                                                                                                          /product= "Human KDR (VEGFR-2) Fab heavy chain (VH)
                                                                                                                                                                                                                                                                                 /note= "CDS does not include start and stop codon"
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Pred. No. 1.3e-57;
0; Mismatches 56
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                                                                                                     Location/Qualifiers
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Best Local Similarity 82.3%;
Matches 288; Conservative
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GOLDSTEIN N I.
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P-PSDB; AAE28870.
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                                                     TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACA
                                                                                                                                                              301 TIGACTACAGGGICTGACTCCTGGGCCCAGGGAGTCCTGGTCACCGTCTC 350
                                                                                                                                                                                  295 GTCACAGATGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTC 344
                                                                                                                                                                                                                                                                                                                                                                 Sequence arrayed library; SAL; 88; antibody library; protein identification; DP47; DPK22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
(KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.
                                                                                                                                                                                                                                                                                                                                           DNA sequence for antibody DP47VH/DPKS22VL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-DEC-2000; 2000JP-0373259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-DEC-2000; 2000JP-0373259
                                                                                                                                                                                                                                                           ABK99212 standard; DNA; 742
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                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel antibody having a first antigen binding stee specific for a first vascular endothelial growth factor (VEGF) receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesse of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treating tumours and for in vivo or in vitro for investigative and diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCTGTGCAGCCTCTG-----GATTCACTTCAGTAGCTATAGCATGAACTGGGTCCGC 114
                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       methods. This polynucleotide sequence represents a human DNA sequence relating to the bispecific antibodies that bind to the VEGF receptors of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                               mitogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAGGTGCAGCTGGTGGAGTCTGGGGGGCGTTGGCAAAGCCTGGGGGGGTCCCTGAGACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New bispecific antibodies having antigen-binding sites specific for first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia
                                                         TIGACTACAGGGICTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                 Grcacagarderriridararcridedeccaadegacaardereacerere 344
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                                                                                                                                                                                                                                                            Cytostatic, antibody, antigen binding site, VEGF receptor, r
leukaemia cell; vascular endothelial growth factor; tumour;
bispecific antigen-binding protein; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 238.4; DB 25;
Pred. No. 1.3e-57;
0; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 348 BP; 82 A; 85 C; 105 G; 76 T; 0 other;
                                                                                                                                                                                                                                   VEGF binding related DNA SEQ ID No 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 70; 98pp; English
                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for treating tumors
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ilarity 82.3%;
Conservative 0
                                                                                                                                                      ABT23325 standard; DNA; 348
                                                                                                                                                                                                                                                                                                                                                                                                  26-JUN-2002; 2002WO-US20332.
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                                                                                                                                                                                                          (first entry)
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P-PSDB; ABJ26763.
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invention relates to screening an antibody against a specific protein
                                                                                                                                                                                                      in an objective structure sample containing a protein group in high efficiency, comprising reacting an objective structure sample containing as protein group or a portion containing an objective protein in the sample with an antibody library, recovering the antibody combined with the protein, replicating the recovered antibody and reacting it with the objective protein at least once. The method is used for the identification of an objective protein. The present sequence is a DNA sequence for an antibody chain (derived from the DP47 heavy chain, the DPK22 light chain or a combination of the two) used in the method of
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Screening of an antibody used for the identification of an objective protein in high efficiency
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 742 BP; 152 A; 186 C; 225 G; 155 T; 24 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                      Example 8; Page 38; 43pp; Japanese.
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Best Local Similarity 80.6
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                   TCCTGTGCAGCCTCTG-----GATTCACCTTTAGTAGTTATGCCATGAGCTGGGTCCGC 122
                                                           CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
                                                                               TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAAACGCCAACAACAACA
                                                                                                                                                      242
                                                                                                                                                                                   CTGTTTCTTCAAATGAACAGCCTGAGAGCTGACACGGCTGTCTATTACTGTGCGAGC 300
                                                                                                                                                                                                              crgrarciecaargaacagrcrgagagccgaggacacggccgrararracrgrgcgaaa 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel method for screening an antibody, comprising performing 2-D electrophoresis on plural proteins in a sample. Individual protein spotes are separated by reacting them with an antibody library and then replicating the bound antibodies before reacting them with the spot proteins again. The method is useful for screening an antibody specific for a target protein, e.g. from a phage antibody library, which is useful in proteomics for studying various protein and complementary decoxyribonucleic acid (CDNA) expression libraries as well as gene functions, and in other biological and medical sciences. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Screening antibody; 2-D electrophoresis; plural protein; protein spot;
                                                                                                                                            TATTATGCAGACTCTGTGAAGGCCCGATTCACCATCTCCAGAGACACTCCAAGAACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screening an antibody using 2-D electrophoresis on plural proteins in samples for separating individual protein spots to react with an antibody library useful in proteomics and other biological sciences -
TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotide is a DNA sequence relating to the antibody screening
                                                                                                                                                                                                                                                                               NNNNNNNNNNNNNTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCC 353
                                                                                                                                                                                                                                              TTGACTACAGGGTCTGACTCCTGGGGGCCAGGGAGTCCTGGTCACCGTCTCC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibody screening method related DNA SEQ ID No 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NISC-) JAPAN SCI & TECHNOLOGY CORP.
(NINA-) JAPAN NAT CENT NEUROLOGY & PSYCHIATRY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody library; proteomics; ds
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66.9%; Score 237; DB 24; Length 742; 80.6%; Pred. No. 3.9e-57;

Query Match Best Local Similarity

other;

Seguence 742 BP; 152 A; 186 C; 225 G; 155 T; 24

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180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, tumour; vascular endothelial growth factor receptor; metastasis; epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC; breast; VEGFR; heart; EGFR; therapy; invasiveness; heavy chain; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibiting tumor growth in humans involves administering vascular endothelial growth factor receptor antagonists in combination with radiation, chemotherapeutic agents, or epidermal growth factor receptor
                                                                                                                                                CAGGCTCCAGGGCAGGGCTGGAGTGTCTCACGTATTAGTAGTAGTGGTGATCCCACA
                            GAGGTGCAGCTGGAGTCTGGGGGCGCCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
                                                          GAGGTGCAGCTGTTGGAGTCTGGGGGGGTTTTGGTACAGCCTGGGGGGGTCCCTGAGACTC
                                                                                       TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC
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/product= "Human KDR (VEGFR-2) Fab heavy chain (VH)
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                                                                                                                                                                                                                                                                                                                                 301 TTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human KDR (VEGFR-2) Fab heavy chain (VH) DNA from D1H4 clone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD46292 standard; DNA; 348
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P-PSDB; AAE28870.
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(IMCL-) IMCLONE SYSTEMS INC.

WPI; 2003-201468/19

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The invention relates to a method of inhibiting tumour growth which involves administering, vascular endothelial growth factor receptor (VEGFR) antagonists in combination with radiation, chemotherapeutic agent, or epidermal growth factor receptor (EGFR) antagonist. The method is useful for inhibiting tumour growth in a human, where the tumour (e.g. tumour of the breast, heart, lung, small intestine, colon, spleen, bone, kidney, bladder, heart, lung, small intestine, colon, spleen, bone, kidney, bladder, heart, uterius, testicles, cervix or liver) over expresses VEGFR. It is also useful for inhibiting growth of colon tumour or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR. It is preferably useful for treating subjects with both solid tumours, preferably high vascular tumours and non-solid tumours. The inhibition of treduction of tumour growth includes prevention or inhibition of the progression of tumour, including cancerous and non-cancerous tumours, where the progression of tumours includes the invasiveness, metaatasis, recurrence and increase in size of the tumour. The present sequence is human KDR (VEGFR-2) Fab antibody heavy chain DNA.
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Sequence 348 BP; 82 A; 86 C; 104 G; 76 T; 0 other;

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TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120
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66.9%; Score 236.8; DB 24; Length 348; 82.0%; Pred. No. 3.6e-57; Indels 6; ive
                  Best Local Similarity 82.0
Matches 287; Conservative
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Cytostatic, antibody; antigen binding site; VEGF receptor; mitogenesis; leukaemia cell; vascular endothelial growth factor; tumour; bispecific antigen-binding protein; human; gene; ds.
                                                                   VEGF binding related DNA SEQ ID No 79
       ABT23327 standard; DNA; 348
                                                (first entry)
                                                                                                                              Homo sapiens
                                                01-MAY-2003
                            ABT23327;
ABT2332
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26-JUN-2002; 2002WO-US20332 26-JUN-2001; 2001US-301299P.

WO2003002144-A1.

09-JAN-2003

Homo sapiens ф

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (VEGF) receptor and a second antigen-binding site specific for a second VEGF receptor. The bispecific antigen-binding proteins block activation of VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treating tumours and for in vivo or in vitro for investigative and diagnostic methods. This polynucleotide sequence represents a human DNA sequence relating to the bispecific antibodies that bind to the VEGF receptors of
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Pred. No. 3.6e-57;
0; Mismatches 57;
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                                                                                                                                                                                                                                                                                                                                            cells, or for treating tumors -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting tumor growth in humans involves administering vascular endothelial growth factor receptor antagonists in combination with radiation, chemotherapeutic agents, or epidermal growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGTGCAGCTGGTGCAGTCTGGGGGGGGCCTGGTCAAGCCTGGGGGGTCCCTGAAACTC
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/*tag= a
/product= "Human KDR (VEGFR-2) Fab heavy chain (VH)
                                                                                                                                                                        protein"
/note= "CDS does not include start and stop codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 12; Page 126; 151pp; English
                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMCLONE SYSTEMS INC. ROCKWELL P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAR-2002; 2002WO-US06762
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Search completed: December 29, 2003, 16:25:40 Job time : 156.453 secs

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Sequence Seq Sequence Sequence Sequence

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Scoring table:

Searched:

Database

No. Result

Perfect score: Sequence:

Run on:

Sequence

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GENERAL INCORDINGS
GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
APPLICANT: KLGETEER, William S.
APPLICANT: NAKAWURA, Takehiko
ITILE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
ITILE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSES: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: Alexandria
STATE: Virgin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCUNTRY: United states

ZIF: Z2313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085
FILING ATTON NUMBER: US/08/803,085
FILING ATTON NUMBER: US/08/803,085
FILING ATTON NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-620
TELEPHONE: (703) 836-2021
TELEPHONE: RESERVERISTICS:
FUNDERMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                         US-08-958-201-5
US-08-45-809A-53
PCT-US93-12501-2
US-08-545-805A-20
US-09-240-274-97
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US-09-36-780-23
US-08-362-780-23
US-08-362-780-23
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US-08-545-809A-9
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Patent No. 6011138
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COUNTRY: United States
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TYPE: nucleic acid
STRANDEDNESS: single
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(without alignments)
4009.823 Million cell updates/sec
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                                                                                                        December 29, 2003, 16:08:50 ; Search time 38.9667 Seconds
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1 GAGGIGCAGCIGGIGGAGIC......ICCIGGICACCGICICCTCA 354
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Sequence 22,
Sequence 48,
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Sequence 11,
Sequence 21,
Sequence 1,
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
              GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-08-652-816A-21
US-08-652-816A-24
US-08-652-816A-24
US-08-652-816A-24
US-08-545-803A-11
US-08-245-803A-21
US-08-026-320A-1
US-08-03-73-83A-11
US-08-545-803A-3
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US-08-428-197-41
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Maximum Match 100%
Listing first 45 summaries
                                                                         OM nucleic - nucleic search, using sw model
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278 ACTACGCAGACTCAGTGAAGGGCAGATTCACCATCTCCAGAGACAATTCCAGAACACGC 337
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                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cirino, Nick M
APPLICANT: Jackson, Paul J
APPLICANT: Jackson, Paul J
APPLICANT: Lehnert, Bruce E
TITLE OF INVENTION: Disruption of Anthrax Toxin Binding to Cell Surface
TITLE OF INVENTION: Receptors
FILE REFERENCE: S-89,662
CURRENT APPLICATION NUMBER: US/09/273,839A
CURRENT APPLICATION NUMBER: 1999-03-22
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 AGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACAT
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TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACAC
                                                                              CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC
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                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/09273839A
Patent No. 6329156
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA 459
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                                                                                     CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
                                                                                                                                                                                                                                                                                                                                                                                     CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGAACACGGCTGTCTATTACTGTGCGAGC 300
                                                                                                                                                                                                                                                                                                                                                                                                         298 CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGC 357
                                                                                                                                            TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: REFF, MITCHELL R.
APPLICANT: BARNET, RICHARD S.
APPLICANT: BARNET, RICHARD S.
APPLICANT: BARNET, RICHARD S.
APPLICANT: MCLACHLAN, KAREN R.
ITILE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES I TITLE OF INVENTION: WESTOOD FOR INTEGRAL SAME SECONDINATION AND TITLE OF INVENTION: WESTOOD FOR ACCOMPLISHING THE SAME FILE REFERENCE: 037003-0275807, CURRENT APPLICATION NUMBER: US/09/343,485A
CURRENT APPLICATION NUMBER: 09/023,715
PRIOR PILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-03-14
NUMBER OF SEQ ID NOS: 3
SOFTWARE PRECENTING OF SEC ID NOS: 3
SEQ ID NO 3
LENGTH: 19040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIFIC SITES
                                                                                                                                                                                                                                                                                                        TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACA
                                                                1 GAGGTGCAGCTGGTGGAGTCTGGGGGGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: referred to as "Mandy" US-09-341-485A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 19040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 95.5%; Score 338.2; DB 4; Length Best Local Similarity 98.9%; Pred. No. 3.8e-95; Matches 351; Conservative 0; Mismatches 3; Indels
      Pred. No. 8.8e-101;
                          ö
                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09343485A; Patent No. 6413777; GENERAL INFORMATION:
    100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                          Matches 354; Conservative
          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-343-485A-3
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        Best Local
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**Gaps** 

181

121

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242 TGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCT 301
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                                                                                                                                                                                                                                                                                                                                                                              296 TIATAAATCCCTACGGTATGGACGTCTGGGCCCAGGGCACCCTGGTCACCGTCTCCTCA 354
                                                                                                                                              Sequence 22, Application US/08652816A
Patent No. 5872215
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Allen, DJ
APPLICANT: Allen, DJ
TITLE OF INVENTION: Specific binding members, materials and TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marahall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CUERTAING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 23-MAY-1996
RIOR APPLICATION NUMBER: 23-MAY-1996
RIOR APPLICATION NUMBER: 02-DEC-1991
RIOR APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
RIOR APPLICATION NUMBER: GB 9206318.9
FILING DATE: 02-DEC-1991
RIOR APPLICATION NUMBER: GB 9206372.6
FILING DATE: 33-SEP-1992
RIOR APPLICATION NUMBER: GB 9206372.6
FILING DATE: 33-SEP-1992
RIOR APPLICATION NUMBER: GB 9206372.6
FILING DATE: 33-SEP-1992
RRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 33-MX-1996
RRIOR APPLICATION DATA:
APPLICATION NUMBER: BCT/GB92/02240
FILING DATE: 02-DEC-1993
RRIOR APPLICATION DATA:
APPLICATION NUMBER: 28111/33308
FILING DATE: 01-UTUN-1994
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 28111/33308
RECOMMUNICATION NUMBER: 28111/33308
RELECOMMUNICATION NUMBER: 28111/46300
RELECOMMUNICATION NUMBER: 28111/46300
RELECOMMUNICATION NUMBER: 28111/46300
RELECOMMUNICATION NUMBER: 28111/46300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Illinois
COUNTRY: United States of America
COUNTUR READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6300 s
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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JS-08-652-816A-22
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Pred. No. 2.6e-59;
0; Mismatches 59; Indel8 12; Gaps
APPLICANT: Allen, DJ
APPLICANT: McCafferty, JG
TITLE OF INVENTION: Specific binding members, materials and TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'TO- STREET: 6300
                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States of America
COUNTRY: United States of America
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 02-DEC-1991
PRIOR APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION NUMBER: GB 9206318.9
FILING DATE: 02-DEC-1991
PRIOR APPLICATION NUMBER: GB 9206372.6
FILING DATE: 03-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 03-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 03-DEC-1995
PRIOR APPLICATION NUMBER: GB 9610824.6
FILING DATE: 03-DEC-1995
PRIOR APPLICATION NUMBER: GB 9610824.6
FILING DATE: 03-DEC-1995
PRIOR APPLICATION NUMBER: GB 9610824.6
FILING DATE: 03-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244.597
FILING DATE: 01-UUN-1994
ATTORNEY, AGENT INPORMATION:
NAME: DATA: NUMBER: 36.107
PRIOR APPLICATION NUMBER: 36.107
PRIOR APPLICATION NUMBER: 36.107
PRIOR APPLICATION NUMBER: 36.107
PRIOR APPLICATION NUMBER: 36.107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 62.3%;
Best Local Similarity 80.2%;
Matches 288; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 354 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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US-08-652-816A-21
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCAGACAATTCCAAGAACAG 234
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                                                                                                                     Gaps
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Sequence 48, Application US/08545809A
BEREAL NO. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Honjo, Tasuku
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                   12;
                                                                                                                                                             1 GAGGTGCAGCTGGTGGAGTCTGGGGGCGCTTGGCAAAGCCTGGGGGGTCCCT
                                                                        Length 354;
                                                                                                                   60; Indels
                                                                    Score 220; DB 2;
Pred. No. 3.9e-59;
0; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MORPHER TARREST DISCRETE

COMPUTER: DISCRETE
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: Fast-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
FILING DATE: 10-MAY-1993
FILING DATE: 10-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRICKALT MOUNT IN ONE TO THE REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 0650
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                      62.1%;
80.0%;
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TYPE: nucleic acid
STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                Matches 288; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
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    ; TOPOLOGY:
US-08-652-816A-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAGGTGCAGCTGGTGGAGTCTGGGGGGGCCTTGGCAAAGCCTGGGGGGGTCCCTGAAACTC
                                                                                                                                                                                                                                            9
                                                                                                                                                                                        Length 743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jequance 24, Application US/08652816A

Patent No. 587215

GENERAL INFORMATION:
APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: Allen, DJ
APPLICANT: Allen, DJ
TITLE OF INVENTION: Specific binding members, materials and
TITLE OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEBE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                     62.0%; Score 219.4; DB 3;
86.0%; Pred. No. 8.4e-59;
iive 0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JMBER: GB 9206318.9
24-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: GB 9206372.6
23-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GB 9125579.8
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
CORGANISM: Homo sapiens
CELL TYPE: human lymphoblast
CELL LINE: CGM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9:
FILING DATE: 02-DEC-1991
                                                                                                                                                                                                                Best Local Similarity 86.0
Matches 257; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB
FILING DATE: 24-MAR-19
PRIOR APPLICATION NUMBER: GB
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.7e-58
      FastSEQ for Windows Version 2.0
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Pred. No. 1.7e-
0; Mismatches
                                                                                                                                                                                                                              06501/004001
                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
                                                                                                                                                                                NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 065/
TELECOMMUNICATION: TELEPHONE: 617-542-8070
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
human lymphoblast
                                                                                                                                                                                                         29,066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 61.7%;
Best Local Similarity 85.9%;
Matches 256; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: Genomic DNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                               TELEX: 200154
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 715 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; CELL TYPE:
; CELL LINE:
US-08-545-809A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS-08-545-809A-21
         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 IGGIGCGCAGCCTCCGGGTTCAGGTTCACCTTCAAIAACTACTACATGGACTGGGTCCGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TCCTGTGCAGCCTCTG-----GATTCACCTTTGATGATTÀTGGCATGAGCTGGGTCCGC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 CAAGCTCCAGGGAAGGGGCTGGAGTGGTCTCTGGTATTAATTGGAATGGTGGTAGCACA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 GGTTATGCAGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGACACGGCTGTCTATTACTGTGCGAGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 CTGTATCTTCAAATGAACAGTCTGAGAGCCGAGGACACAGCCGTGTATTACTGTGCAAGA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAGGTGCAGCTGGTGGAGTCTGGGGAGGTGTGGTACGGCCTGGGGGGTCCCTGAGGCTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11. Application US/08545809A

Patent No. 6096878

GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Mateuda, Punkhiko
TITLE OF INVENTION: BEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 TTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 AGGCGGTATGCGTTGCATTATTGGGCCAAGGTACCCTGGTCACCGTGTC 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAGGIGCAGCIGGIGGAGICIGGGGGGGGGCTIGGCAAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .9e-59;
les 68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 6.96
0; Mismatches
PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23 MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATYONREY/GBRY INFORMATION:
NAME: DAVIG W. CLOUGH
REGISTRATION NUMBER: 36,107
REFRENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.9%; Score 219.2; ilarity 78.9%; Pred. No. 6.9 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 348 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette
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MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
OPERATING SYSTEM: Wi
                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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Best Local Similarity
Matches 276; Conserv
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ZIP: 02110-2804
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CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
US-08-652-816A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-08-545-809A-11
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361 AGGIGCAGCIGGIGGAGICIGGGGGAGGCIIGGICAAGCCIGGAGGGICCCIGAGACTCI 420
                                                                                                                                                                                                                                                             62 GGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCC 121
                                                                                                                                                                                                                                                                                                                                  421 ccrigricosoccricric ---- Garricaccririca Gracia Cracia Garganica de 174
                                                                                                                                                                                                                                                                                                                                                                                                        122 AGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            535 ACTACGCAGACTCTGTGAAGGGCCGATTCACCATCTCCAGGGACAAGGAAGTCAC 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 TGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 TGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAG 652
                                                                                                                                   2 AGGTGCAGCTGGTGGAGTCTGGGGGCCGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HONGO, Taguku
APPLICANT: Matguda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
CORRESPONDENCES: 145
ADDRESSEE: Fish & Richardson, P.C.
                                                                 9
Length 715;
                                                              Indels
DB 3;
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LOCATION: 1..432
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 GAGGIGGAACIGGAGICTGGGGGAGGCCIGGICAAGCCIGGGGGGGCCTGAGACIC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 rccrcrcrccaccrcrc-----Garrcaccrrcagragerarageargaacrccc 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 CAGGCTCCAGGCCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTAGTAGTAGTTACTACATA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAGGTGCAGCTGGTGGAGTCTGGGGGGGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIGIATCTGCAAAIGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGA 461
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Sequence 1, Application US/08026320A

GENERAL INFORMATION:
APPLICANT: Irie, Reiko F
TITLE OF INVENTION: HUMAN B-LYMPHOBLASTOID CELL LINE
TITLE OF INVENTION: BECRETING ANTI-GANGLIOSIDE ANTIBODY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Poms, Smith, Lande & Rose
STREET: 2029 Century Park East, Suite 3800
CITY: Los Angeles
STREET: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 217.8; DB 3; Length Pred. No. 2.3e-58;
0; Mismatches 37; Indels
OPERATING SYSTEM: Windows95
SOCTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCEY/DOCKET NUMBER: 29,066
REFERENCEY/DOCKET NUMBER: 20,066
REFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 200154
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 519 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
CELL TYPE: human lymphoblast
CELL LINE: CGM1
US-08-545-809A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 85.6%;
Matches 256; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-08-026-320A-1
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58 GAGGTGCAGCTGTTGGATTCTGGGGGGCTTGGTACAGCCTGGGGGGGCCTGAGACTC 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 CAGGCTCCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 cagecrecadedaaagageergaagragarerekaerarraargagragrageaagaa 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function= "Heavy Chain"
/product= "Immunoglobulin Variable Region"
/standard_name= "HuMab L612 Heavy Chain Variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAGGTGCAGCTGGTGGAGTCTGGGGGCGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature;
i.CCATION: 397..429
COTHER INFORMATION: /function= "Complementary determining;
CTHER INFORMATION: region 3 (CDR3)"
US-08-026-320A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indele
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CELL TYPE: Epstein Barr Virus Transformed B cell
CELL LINE: L612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            determining region 1 (CDR1) "
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LOCATION: 271...300
OTHER INFORMATION: /function= "Complementary
OTHER INFORMATION: determining region 2 (CDR2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 60.9%; Score 215.6; DB 1; Best Local Similarity 79.0%; Pred. No. 1e-57; Matches 289; Conservative 0; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function= "Complementary
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/026,320A
FILING DATE: 26-FEB-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/609803
FILING DATE: 05-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J
REGISTRATION NUMBER: 29421
REFERENCE/DOCKET NUMBER: 94268
TELECOMMUNICATION INFORMATION:
TYPE: nucleic acid
TYPE: DOLOGY: linear
MOLECULE TYPE: CDNA
HYDOTHETICAL: NO
ANTIL SENSE: NO
ANTIL SENSE: NO
ORGINAL SOUNCE:
ORGANISM: HOMO SADIENS
TRAIL TYPE: EDSTEIN BAIR VIRUS TIAN
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LOCATION: 148.762
OTHER INFORMATION: /fur
OTHER INFORMATION: dete
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                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/09273839A

Sequence 11, Application US/09273839A

Patent No. 632916

GENERAL INFORMATION:

APPLICANT: Cirino, Nick M

APPLICANT: Jehnert, Bruce E

TITLE OF INVENTION: Disruption of Anthrax Toxin Binding to Cell Surface

TITLE OF INVENTION: Receptors

FILE REFERENCE: S-89,662

CURRENT APPLICATION NUMBER: US/09/273,839A

CURRENT PILING DATE: 1999-03-22

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 11

LENGTH: 892
                                                                                    ------GCTTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACGTC 348
                                                                                                           352 GGTGGCAACGATTTTTGACTGGTTATTATGCTTGGGGCCAGGGAACCCTGGTCACCGTC 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 GTTATGCAGACTCTGTGAAGGGCCGATTCGCCGTCTCCAGAGACACACGCCAAGAACTCCC 337
241 CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGA-- 298
                         292 TTGTATCTGCAAATGAACAGCCTGAGAGGCGGAGGACACGGCCGTATATTACTGTGCGAAA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACAC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCT 301
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APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REPERENCE: PFF50
CURRENT APPLICATION NUMBER: US/10/039,785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9;
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US-10-039-785-65
; Sequence 65, Application US/10039785
; Patent No. 6538938
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Best Local Similarity 79.5%;
Matches 283; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-273-839A-11
                                                                                                                                                                         TCCTCA 354
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US-09-273-839A-11
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61 TGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 TGGTACGCAGACTCCGTGAAGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 cagecrecagecaagegeriegagregererekeerarragregragregrageaa 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 CTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAGGTGCAGCTGGTGGAGTCTGGGGGGGCGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-545-809A-23
Sequence 23, Application US/08545809A
Sequence 23, Application US/08545809A
Sequence 23, Application Sequence 23, Application US/08545809A
Sequence 23, Application Sequence 23, Applicant Material Period Funition Factor Material Period Funition Figure 11TLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME NUMBER OF SEQUENCES: 145
CORRESPONDENCE Figh & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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Pred. No. 2.6e-57;
0; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: DNA encoding T1006F07 scFv
US-10-039-785-65
PRIOR FILING DATE: 2002-04-05
PRIOR PILING DATE: 2000-12-20
PRIOR PILING DATE: 2000-12-20
PRIOR PILING DATE: 2001-12-20
PRIOR PILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-08-04
PRIOR FILING DATE: 2001-08-05
PRIOR FILING DATE: 2001-08-05
PRIOR FILING DATE: 2001-08-05
PRIOR FILING DATE: 2001-08-05
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-05
PRIOR PLING DATE: 2001-06-05
PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR 
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Best Local Similarity 84.9%;
Matches 254; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 225 | CITY: Boston
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MEDIUM TYPE: 1 EPOPY disk
COMPUTER: 1 BM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,197
FILING DATE:
FILING DATE: 20-0CT-1993
ATTORNEY/AGBNT INPORMATION:
NAME: Howells, Stacy L.
REFERENCE/DOCKET NUMBER: PC-2630
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5100
SEQUENCE CHARATICE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 351 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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CLONE: SpA3-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY:
; LOCATION:
US-08-428-197-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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CORRESPONDENCE ADDRESS:
STOOMESSEE: Spension: Stoomstoom Stoomstoom Stoomstooms Stooms Stoom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 GAGGTGCAGCTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGTGCGCACCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 TCCTGTGCAGCCTCTG-----GATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGC 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTAGTGGTGATCCCACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 TGGTACGCAGACTCCGTGAAGGCAGATTCACCATCTCCAGAGAGACGCCAACAACACAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACACAATTCCAAGAACACG 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 CTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGA 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAGGTGCAGCTGGTGGAGTCTGGGGGCGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
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Pred. No. 4.5e-57;
0; Mismatches 39; Indels 6
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            06501/004001
                                                                                                                            PADLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
RIOR APPLICATION DATE:
APPLICATION DATE:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 35, Application US/08428197
Patent No. 5891438
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
CELL TYPE: human lymphoblast
CELL LINE: CGM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 200154
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 514 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 60.3%;
Best Local Similarity 84.9%;
Matches 253; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-545-809A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-08-428-197-35
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DNA (genomic)

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APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ccadedaadedecredacrederreterantratretedaacreteraracratacrac 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 CTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTGAC- 305
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                                                                                                                                                                                                                                                       67 GCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAGGCT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 GCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGGAACGCCAACAACACACTGTTT 246
                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                      67 GAAGCCTCTG-----GATTCCCCTTCAGTAACTATGGCATGAGCTGGGTCCGCCAGGCT
                                                                                                                           7 CAGCTGGTGGAGTCTGGGGGGGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTCTGGTGC
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                                                               Gaps
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                                                            6
Length 351;
                                                            Indels
Score 212.2; DB 2;
pred. No. 1e-56;
0; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US93-10555-35; Sequence 35, Application PC/TUS9310555; GENERAL INFORMATION:
   59.9%;
Query Match
Best Local Similarity 79.5
Matches 279; Conservative
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E: Spensley Horn Jubas & Lubitz 1880 Century Park East - Suite 500

CITY: Los Angeles STATE: California COUNTRY: USA

STREET:

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181 GCCGACTCCGTGAAGGCCGGTTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 CCAGGGCAGGGGTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGGTAC 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 GCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAGGCT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTGAC- 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGCCTCTG-----GATTCCCCTTCAGTAACTATGGCATGAGCTGGGTCCGCCAGGCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 CTGCTCGAGGAGTCTGGGGGGGTGGCTTGGTACAGCCTGGGGGTGCCCCTGAGACTCCTCCTGT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 CAGCTGGTGGAGTCTGGGGGCGCGTTGGCAAAGCCTGGGGGGGTCCCTGAGACTCTGGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.9%; Score 212.2; DB 5; Length 351; 79.5%; Pred. No. 1e-56; Live 0; Mismatches 63; Indels 9
                                                                                                               COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/10555

FILING DATE: 29-OCT-1993

CLASSIFICATION: COMPATION:

NAME: Howells, Stacy L.

REGISTRATION NUMBER: PC-2630

TELEPANCE (619) 455-5100

TELEPANCE (619) 455-5100

TELEPANCE (619) 455-5100

TELEPANCE CHARACTERISTICS:

LENGTH: 351 base pairs

TYPE: MUCLEIC ACID
                       1880 Century Park East - Suite 500
Spensley Horn Jubas & Lubitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 79.5
Matches 279; Conservative
             STREET: 1880 CITY: Los Angeles caty: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US93-10555-35
ADDRESSEE:
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Search completed: December 29, 2003, 21:48:31 Job time : 39.9667 secs

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Appli Appli

Appl Appl Appl Appl Appl Appl

Scoring table:

Searched:

Database

Perfect score:

Sequence:

OM nucleic

Run on:

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Sequence
Sequence 86,
Sequence 60, App.
Sequence 17, Appl
Sequence 31233, A
Sequence 90, Appl
Sequence 58, Appl
Sequence 58, Appl
                                                                                                                Sequence 118, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 191,
                                                                                                                                   Sequence 102,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 82,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09019441
Publication No. US20030086921A1
GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
KLOSTZER, William S.
NAKAMURA, Takehiko
TITLE OF INVENTION: AMMILAN ANTI-HUMAN CD23 MONOCLONAL
ANTIBODIES AND USE THEREOF AS THERAPEUTICS
                                                                          Sequence
                                                                                                                                                                                                                                Sequence
                                                                                                                                                       Sequence
                                                                                                                                                                                            Sequence
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                                       Sequence
                                                                                                                                                                       Sequence
                                                          Sequence
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
STREET: P.O. Box 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version #1.30
US-09-969-748C-1

US-10-309-764-134

US-10-309-764-70

US-10-309-764-70

US-10-309-764-70

US-10-309-764-70

US-10-309-764-102

US-10-309-764-102

US-10-309-764-102

US-10-309-764-102

US-10-309-764-10

US-10-309-764-66

US-10-309-764-66

US-10-309-764-66

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US-10-309-764-66

US-10-309-764-86

US-10-309-764-90

US-10-309-764-86

US-10-309-764-80

US-10-309-764-80

US-10-309-764-80

US-10-309-764-80

US-10-309-764-80

US-10-309-764-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Virginia
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIble
COMPUTER: IBM PC COMPATIble
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,441
FILING DATE: 05-Feb-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
       US-09-019-441-4
                                                                                                                                                     221.8
221.8
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       Sequence 4, Appl:
                                                                                                                                   December 29, 2003, 19:01:43 ; Search time 511.438 Seconds (without alignments) 2371.523 Million cell updates/sec
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Sequence 96, A
Sequence 130,
Sequence 126,
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                                                                                                                                                                                                                                      354
1 GAGGTGCAGCTGGAGTC......TCCTGGTCACCGTCTCCTCA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
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(cgn2_6/ptodata/2/pubpna/US06_WEW_PUB.seq:*
(cgn2_6/ptodata/2/pubpna/US06_WEW_PUB.seq:*
(cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
(cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
(cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
(cgn2_6/ptodata/2/pubpna/DSOB_WEW_PUB.seq:*
(cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
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(cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
(cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
(cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
(cgn2_6/ptodata/2/pubpna/USOB_WEW_PUB.seq:*
(cgn2_6/ptodata/2/pubpna/USOB_WEW_PUB.seq:*
(cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
(cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
(cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
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(cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
(cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
(cgn2_6/ptodata/2/pubpna/USOB_WEW_PUB.seq:*
(cgn2_6/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
(cgn2_6/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
(cgn2_6/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
(cgn2_6/ptodata/2/pubpna/USOB_NEW_PUB.seq:*
                         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-091-300-23
US-10-091-300-27
US-10-291-265-99
US-10-291-265-96
US-10-309-764-130
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US-10-103-686-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                    - nucleic search, using sw model
                                                                                                                                                                                                                  US-09-019-441-4_COPY_58_411
                                                                                                                                                                                                                                                                                           IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:

Sequence 6 Sequence 6

US-10-309-764-126 US-10-322-673-66 US-10-322-673-68 US-09-949-039-1

Score

Result No.

Sequence

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118 regrececescerecegerreagerreacerrearraceracargaacregerees 177
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Patent No. US20020068276A1

GENERAL INFORMATION:

APPLICANT: Winter, Greg

TITLE OF INVENTION: Methods for Selecting Functional Peptides

TILE REPERENCE: 3789/72916

CURRENT APPLICATION NUMBER: US/09/192,854

CURRENT PEPLING DATE: 1998-11-17

EARLIER APPLICATION NUMBER: 60/066,729

SARLIER PILING DATE: 1997-11-21

NUMBER OF SEQ ID NOS: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAGGTGCAGCTGGTGGAGTCTGGGCGCGCTTGGCCAAAGCCTGGGGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 354; DB 15; 100.0%; Pred. No. 4.6e-102;
                           ALLOWARD TOWNS TO THE ROBIN L. REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 58.7411
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                  INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                   mat_peptide
58..411
                                                                                                                                                                                                                                                                                                                                             1..411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 354; Conservative
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SEQ ID NO 1
LENGTH: 720
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US-09-192-854-1
                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
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Publication No. US20030059424A1
GENERAL INFORMATION: Atchell E.
KLOETZER, William S.
NAKAMURA, TAKehiko
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
ANTIBODIES AND USE THEREOF AS THERAPEUTICS
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                                                                                                                                                                                                                                                                                                        Length 411;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSES: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                   100.0%; Score 354; DB 11;
100.0%; Pred. No. 4.6e-102;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States
COUNTRY: United States
CONTRY: United States
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/10/103,686 FILING DATE: 25-Mar-2002 CLASSIFICATION: «UNKNOWN» PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/803,085
                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-09-019-441-4
                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                   NAME/KEY: mat_peptide
SEQUENCE CHARACTERISTICS:
LENGTH: 411 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                 1..411
                                                                                                                                                                                                                                                                                                                                             Matches 354; Conservative
                                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                            LOCATION:
                                                                                                                                                                                  FEATURE
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GENERAL INCRMANTION:

GENERAL INCRMANTION:

APPLICANT: Winter, Gregory

TITLE OF INVERTURION: Method to Screen Phage Display Libraries with Different Ligands
FILE REPRENCE: 8039/1073

CURRENT APPLICATION NUMBER: US/09/968,744A

CURRENT APPLICATION NUMBER: US/09/968,744A

CURRENT APPLICATION NUMBER: US/09/968,744A

FILE REPRENCE: 1997-10-20

FRIOR APPLICATION NUMBER: US/00/65,248

FRIOR FILING DATE: 1997-11-13

FRIOR FILING DATE: 1997-11-13

FRIOR APPLICATION NUMBER: US/00/66,729

FRIOR APPLICATION NUMBER: US/00/66,729

FRIOR APPLICATION NUMBER: US/00/66,729

FRIOR APPLICATION NUMBER: US/00/66,729

FRIOR PILING DATE: 1998-10-20

FRIOR FILING DATE: 2000-0-24

NUMBER OF SEQ ID NOS: 350

SOFTWARE: PARENT NESTON NUMBER: PARENT NUMBER: PARENT NUMB
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                                                                                                                              175 racracecaeacrecereaaeeeceerreacearereceaeaeaacaarrecaagaacaee 234
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                                                                                                                                                                                                                                                        61 recreredededecreta----darreacerrrageacrareceareacresereded 114
115 CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACA 174
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                                                                                                                                                                                                                                                                                                                            301 TTGACTACAGGGTCTGACTCCTGGGCCAGGGAGTCCTGGTCACCGTCTC 350
                                                                                                                                                                                                                                                                                                                                                                            295 AGTTATGGTGCTTTTGACTACTGGGGCCAGGAACCCTGGTCACGTCTC 344
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Pred. No. 7e-66;
0; Mismatches 5
                                                                    181 TGGTACGCAGACTCCGTGAAGGGCAGATTCACCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09968744A; Publication No. US20030148372A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 82.6%;
Matches 289; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-968-744A-1
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APPLICANT: Tomilison, Ian M
APPLICANT: Winter, Gregory
ITIAL Minter, Gregory
FILE REPERBNCE: 8039/10738
CURRENT APPLICATION NUMBER: US/09/968,561A
CURRENT FILING DATE: 2001-10-01
PRIOR PILING DATE: 1997-10-20
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
PRIOR PLING DATE: 1997-11-13
PRIOR PLING DATE: 1997-11-13
PRIOR PLING DATE: 1997-11-31
PRIOR PLING DATE: 1998-10-20
PRIOR PLING DATE: 2000-02-4
NUMBER OF SEQ ID NOS: 350
SSOFTWARE: PATENT VERSION 3.1
LENGTH: 720
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82.6%; Pred. No. 7e-66;
ive 0; Mismatches 55; Indels
                                        Length 720;
                                                                                                      55; Indels
                                     Score 240; DB 9;
Pred. No. 7e-66;
                                                                                                      0; Mismatches
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                                        67.8%;
82.6%;
                                        Query Match
Best Local Similarity 82.6'
Matches 289; Conservative
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ORGANISM: Homo sapiens
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Sequence 30. Application US/10091300
Publication No. US20030108545A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rockwell, Patricia
APPLICANT: Goldstein, Neil I.
ITILE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular
ITILE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
FILE REFERENCE: 11245,46211
CURRENT APPLICATION NUMBER: US/10/091,300
CURRENT FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: WordPerfect 8.0 for Windows
SECTION 300
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Matches 286; Conservative
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; ORGANISM: Human
US-10-091-300-30
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US-10-091-300-30
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RESULT 6
US-10-091-300-23
Sequence 23, Application US/10091300
Publication No. US20030108545A1
GENERAL INFORMATION:
APPLICANT: Gockwell, Patricia
TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular;
TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
CURRENT APPLICATION NUMBER: US/10/091,300
CURRENT FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: WordPerfect 8.0 for Windows
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US-10-091-300-27
US-10-091-300-27
Sequence 27, Application US/10091300
Fublication No. US20030108545A1
GENERAL INFORMATION:
APPLICANT: Rockwell, Patricia
TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
CURRENT APPLICATION NUMBER: US/10/091,300
CURRENT FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: WordPerfect 8.0 for Windows
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGTACGCAGACTCCGTGAAGGCAGATTCACCATCTCCAGAGAGAACGCCAACACACA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 CTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGGA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATTAGTAGTAGTAGTAGTAATA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 TACTACGCAGACTCAGTGAAGGGCCGATTCACCATCTCCAGAGAACAACGCCAAGAACTCA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGTTTCTTCAAATGAACAGCCTGAGAGCTGACACGCTGTCTATTACTGTGCGAGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAGGTGCAGCTGCTGCAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGGTCCCTGAGACTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAGGTGCAGCTGGTGGAGTCTGGGGGCGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 TIGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 GTCACAGATGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTC 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 238.4; DB 15; Length
Pred. No. 1.9e-65;
0; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.9%; Score 236.8; DB 15; Length
82.0%; Pred. No. 6e-65;
ive 0; Mismatches 57; Indels
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Best Local Similarity 82.0
Matches 287; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 82.3
Matches 288; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Human
US-10-091-300-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Hur
US-10-091-300-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 23
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Best Local S
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APPLICANT: Foltz, Jan
APPLICANT: Babcock, John
APPLICANT: Babcock, John
APPLICANT: Poltz, Jan
APPLICANT: Poltz, Jan
APPLICANT: Palathumpat, Raju
APPLICANT: Palathumpat, Raju
APPLICANT: Wang, Chadwick T.
TITLE OF INVENTION: ANTI-CDR45RB ANTIBODIES FOR USE IN
TITLE OF INVENTION: ANDIBER: US/10/309,764
CURRENT APPLICATION NUMBER: 60/337,276
PRIOR APPLICATION NUMBER: 60/337,276
PRIOR APPLICATION NUMBER: 60/337,276
PRIOR APPLICATION NUMBER: 60/337,276
PRIOR APPLICATION NUMBER: 60/337,276
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   393 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACG 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279 TCCTGTGCAGCCTCTG-----GATTCACCTTTAGCAGTTTTTCGATGAGCTGGGTCCGC 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        453 crerarcrecaaareaacaeccreaeaecceaeeacaceeccerararracrereceaaa 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 TIGACTACAGGGTCTGACTCCTGGGGCCCAGGGAGTCCTGGTCACCGTCTC 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             513 ccerrrecerarrradacracresseccassedaaccersercaccerere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 235.2; DB 12;
Pred. No. 3e-64;
0; Mismatches 58;
                             PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR PILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 130, Application US/10309764
Publication No. US20030232009A1
GENERAL INFORMATION:
APPLICATION NUMBER: 09/617,746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.0%;
82.3%;
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Best Local Similarity 81.7%;
Matches 286; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (162)..(1085)
US-10-291-265-96
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ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                                     Sequence 99, Application US/10291265
Publication No. US20030232054A1
GENERAL INFORMATION:
TEMBEL INFORMATION:
TITLE NOT INTO TOTAL T
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Publication No. US20030232054A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tang et al
TITLE OF INVENTION: No. US20030232054A1e1 Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
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Pred. No. 3e-64;
0; Mismatches 58; Indels
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Best Local Similarity 81.7
Matches 286; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (162) .. (1253)
US-10-291-265-99
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US-10-291-265-96
                                                                                US-10-291-265-99
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293 TGTTTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAA 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGGACGCCAACAACACAC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 actacecaeacteceteaacececestreacearetecaacaattecaacaacaacace 235
                        233 ACTACGCAGACTCTGTGAAGGGCCGATTCACCATCTCCAGGGACAACGCCAAGAACTCAC 292
                                                                      301
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Sequence 66, Application US/10322673

Publication No. US2003018029641

GENERAL INFORMATION:
APPLICANT: Salced tal.
TITLE OF INVENTION: Receptors
TITLE OF INVENTION: Receptors
FILE REFERENCE: PF988
CURRENT APPLICATION NUMBER: US/10/322,673

CURRENT FILING DATE: 2002-12-19

PRIOR PILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 60/369,877

PRIOR PILING DATE: 2002-04-05

PRIOR APPLICATION NUMBER: 60/384,828

PRIOR APPLICATION NUMBER: 60/384,828

PRIOR PILING DATE: 2002-06-04

PRIOR FILING DATE: 2002-06-04

PRIOR PILING DATE: 2002-07-18

PRIOR PILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/403,370

PRIOR PILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/403,370

PRIOR PILING DATE: 2002-07-18

PRIOR PILING DATE: 2002-07-18

PRIOR PILING DATE: 2002-07-18

PRIOR PELICATION NUMBER: 60/403,370

PRIOR PILING DATE: 2002-07-18

                                                                                                                                                               TGAC-----TACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCT
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: DNA encoding CM087C06 scFv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 65.3%;
Best Local Similarity 81.1%;
Matches 283; Conservative
                                                                                                                                                                                                                                                                CA 354
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                                                                                                                                                                          233 ACTACGCAGACTCTGTGAAGGGCCGATTCACCATCTCCAGGGACAATGCCAAGAACTCAC 292
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                                                                                                                                               62 GGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCC 121
                                                                                                                                                                                                                                          AGGCTCCAGGGCCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACAT 181
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APPLICANT: Babcook, John
APPLICANT: Babcook, John
APPLICANT: Babcook, John
APPLICANT: Babcook, John
APPLICANT: Palathumpat. Raju
APPLICANT: Yang, Xiao-dong
APPLICANT: Xing, Chadwick T.
TITLE OF INVENTION: ANTI-CDR45RB ANTIBODIES FOR USE IN
TITLE OF INVENTION: TEATING AUTOIMMUNE DISEASE AND TRANSPLANT REJECTION
FILE REFERENCE: ABGENIX.029A
CURRENT APPLICATION NUMBER: US/10/309,764
CURRENT APPLICATION NUMBER: 60/337,276
PRIOR APPLICATION NUMBER: 60/337,276
                                                                                                 59 AGGIGCAGCIGGIGGAGICIGGGGGGGGCTIGGTCAAGCCIGGAGGGICCCIGAGACTCI
                                                     2 AGGTGCAGCTGGTGGAGTCTGGGGGGCCGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTCT
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Pred. No. 2.1e-63;
0; Mismatches 50; Indels 15;
         15;
         49; Indels
         0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 126
LENGTH: 414
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Best Local Similarity 82.0%;
Matches 297; Conservative
         298; Conservative
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US-10-309-764-126
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FILE REFERENCE: 057220/1301
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APPLICANT: HAWLEY, STEPHEN B.
TITLE OF INVENTION: COMPOUNDS AND MOLECULAR COMPLEXES COMPRISING MULTIPLE; TITLE OF INVENTION: BINDING REGIONS DIRECTED TO TRANSCYTOTIC LIGANDS
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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296 GAGGATCCACTTTTGATATCTGGGGCCGGGGGACAATGGTCACCGTCTC 344
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Pred. No. 7.8e-63;
0; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: DNA encoding CM085C11 scFv
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 65.1%;
Best Local Similarity 80.9%;
Matches 283; Conservative
                                                        RESULT 14
US-10-322-673-68
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US-09-949-039-1
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                                                                                                                                                                   Description of Artificial Sequence: pSyn5AF DNA sequence
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Pred. No. 5.3e-62;
0; Mismatches 56
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Job time : 513.438 secs
CURRENT APPLICATION NUMBER: US/09/949,039
CURRENT FILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 81.7%;
Matches 291; Conservative C
                                                                                                                                                                               OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                       LENGTH: 4026
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